

u89336exon#54_51-
 369:not_in_gb_record,_unknown_gene_extracted_fromhla_iii_region_containing_notch4_g
 u89336exon#65_12-282:in_reversesequence,_54136-
 54166:not_in_gb_record,_unknown_gene_extracted_fromhl
5 u92436_2591-3077,mutated_in_multiple_advanced_cancers_protein_(mmac1)_mrna,_complete_cds.
 x03072cds_765-1089:in_reversesequence,_3505-3649,int-1_mammary_oncogene_
 x04707cds_815-1343:in_reversesequence,_1649-1673,c-erb-a_mrna_for_thyroid_hormone_receptor
 all_x07203_1419-1576,mrna_for_cd20_receptor_(s7)_
 all_x16866_688-1280,mrna_for_cytochrome_p-450iid_(clone_pmp33)_
10 all_x51823_2-51,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_(_partial)/gb=x51823_/ntype=rn
 x52008cds_899-1325:in_reversesequence,_1748-1814,alpha-
 2_strychnine_binding_subunit_of_inhibitory_gi
 x58431mrna#1_1781-2299,_hox_2.2_gene_extracted_fromhox2.2_gene_for_a_homeobox_protein_
15 x61072mrna_43-325,mrna_for_t_cell_receptor,_clone_igra17.
 all_x62466_25-410,mrna_for_campath-1_(cdw52)_antigen_
 all_x68314_466-923,mrna_for_glutathione_peroxidase-gi
 x80923mrna_31-361,nov_gene/gb=x80923_/ntype=dna/_annot=mrna
 all_x89059_722-1203,mrna_for_unknown_protein_expressed_in_macrophages
20 x90763_1272-1632,mrna_for_type_i_keratin,_hha5_
 x91103cds_587-965:in_reversesequence,_1055-1097,mrna_for_hr44_protein/gb=x91103_/ntype=rna
 all_z11737_1537-2120,mrna_for_flavin-containing_monomooxygenase_4
 z15114cds_1319-1589:in_reversesequence,_1595-
 1805,mrna_for_protein_kinase_c_gamma_(partial)_
25 all_z48482_2998-3401,mrna_for_membrane-type_matrix_metalloproteinase_2_
 all_z80783_510-565,h2b/l_gene
 all_z83336_618-702,hh2b/d_gene.
 z83821cds#2_1428-1668:in_reversesequence,_39964-
 40156,dna_sequence_from_pac_296k21_on_chromosome_x_c
30
 Metagene 433

 af000573mrna_1162-1666,homogentisate_1,2-dioxygenase_gene,_complete_cds.
 d45399mrna_155-
35 629,adult_neural_retina_mrna_forcone_cgmp_phosphodiesterase_gamma_subunit,_complete_c
 hg4557-ht4962_r_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_1snrp_
 k03189cds_2-404,chorionic_gonadotropin_beta_subunit_gene_
 all_l43579_398-
 428,(clone_110298)_mrna/gb=l43579_/ntype=rna,(clone_110298)_mrna/gb=l43579_/ntype=rna

all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 m60828_3252-3720,keratinocyte_growth_factor_mrna,_complete_cds_
 s76853_1683-2244,_cerebrin-

5 50=cerebrospinal_fluid_protein_[human,_cerebral_brain,_mrna,_2295_nt]
 u43189_2384-2942,ets_transcription_factors_nerf-1a_and_nerf-1b_(nerf-1a,b)_mrna,_complete_cds
 v00571mrna_714-1218,gene_encoding_prepro_form_of_corticotropin_releasing_factor_
 all_x04571_4306-4835,mrna_for_kidney_epidermal_growth_factor_(egf)_precursor_
 x61755mrna_1020-1562,hox3d_gene_for_homeoprotein_hox3d

10 all_x66403_1856-2301,mrna_for_acetylcholine_receptor_(epsilon_subunit)_
 x80695cds_938-1250:in_reversesequence,_1298-1496,oxalhs_mrna_
 all_z22535_2433-2932,alk-3_mrna
 z50781cds_100-205:in_reversesequence,_346-394,mrna_for_leucine_zipper_protein_

15 Metagene 320

d17400_196-622,mrna_for_6-pyruvoyl-tetrahydropterin_synthase,_complete_cds_
 d38498_37-604,pms5_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-terminal_region)

20 hg3991-ht4261_r_at_hg3991-ht4261_cpg-enriched_dna_clone_e18_
 j05500mrna#1_6200-6740,beta-spectrin_(sptb)_mrna,_complete_cds_
 l13689mrna_2674-3076,prot-oncogene_(bmi-1)_mrna,_complete_cds
 u18291_1439-1973,cdc16hs_mrna,_complete_cds
 u22662_1017-1473,nuclear_orphan_receptor_lxr-alpha_mrna,_complete_cds

25 u35100_330-915,complexin_ii_mrna,_complete_cds.
 x05855cds_12-65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
 all_x63597_5486-5979,si_mrna_for_sucrase-isomaltase
 all_x68486_2465-2934,mrna_for_a2a_adenosine_receptor_
 all_z23091_6853-7358,gpv_gene_encoding_platelet_glycoprotein_v_precursor

30 Metagene 246

hg2380-ht2476_s_at_hg2380-ht2476_adp-ribosylarginine_hydrolase_
 m35252_602-998,co-029

35 u59325_2353-2815,cadherin-14_mrna,_complete_cds
 y12812cds_486-768:in_reversesequence,_914-1130,rfxap_mrna_

Metagene 46

af000424_214-610,1st1_mrna,_clst1/c_splice_variant,_complete_cds
 d30036_1743-2283,mrna_for_phosphatidylinositol_transfer_protein_(pi-talpha),_complete_cds_
 d64109_642-1152,mrna_for_tob_family,_complete_cds
 111672_3266-
5 3562,kruppel_related_zinc_finger_protein_(htf10)_mrna,_complete_cds,kruppel_related_zinc
 115326_2760-3323,endoperoxide_synthase_type_ii_mrna,_complete_cds
 m27543mrna_2548-3070,guanine_nucleotide-
 binding_protein_(gi)_alpha_subunit_mrna,_complete_cds
 m29335_2-180,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-alpha_mrna,_partial_cds
10 m95178_2567-2996,non-muscle_alpha-actinin_mrna,_complete_cds_
 u37248_848-1304,alpha-mannosidase_(6a8)_mrna,_complete_cds_
 u42387_1180-1642,pancreatic_polypeptide_receptor_mrna,_complete_cds
 u49957_5044-5581,lim_protein_(lpp)_mrna,_partial_cds_
 u66661_2656-3082,gaba-a_receptor_epsilon_subunit_mrna,_complete_cds
15 u77665_393-873,rnasep_protein_p30_(rpp30)_mrna,_complete_cds.
 u78524_1571-1967,gu_binding_protein_mrna,_partial_cds
 u90904_1102-1342,clone_23773_mrna_sequence_
 x01630cds_883-1213:in_reversesequence,_1312-1468,mrna_for_argininosuccinate_synthetase
 x04143cds_49-265:in_reversesequence,_1430-1592,gene_for_bone_gla_protein_(bgp)
20 all_x16832_840-1381,mrna_for_cathepsin_h_(ec_3.4.22.16)
 all_x54936_1140-1627,mrna_for_placenta_growth_factor_(plgf)
 all_x70683_2322-2752,mrna_for_so_4_protein
 all_x85545_1122-1591,mrna_for_protein_kinase_pkx1_
 all_x90392_2058-2545,mrna_for_dnase_x_gene_
25
 z32765exon_79-159,cd36_gene_exon/gb=z32765/_ntype=dna/_annot=exon

Metagene 318

30 hg3111-ht3287_at_hg3111-ht3287_autoantigen_
 m57230_2652-3000,membrane_glycoprotein_gp130_mrna,_complete_cds
 all_x68487_1174-1667,mrna_for_a2b_adenosine_receptor_
 all_x89430_1828-2333,mrna_for_methyl_cpg_binding_protein_2_
 z18951cds_311-509:in_reversesequence,_627-813,mrna_for_caveolin_

35

Metagene 424

hg311-ht311_at_hg311-ht311_ribosomal_protein_l30_
 m26167mrna_385-730,platelet_factorvariation(pf4var1)_gene,_complete_cds

m28219_7-

253,low_density_lipoprotein_receptor_(fhlmutant_causing_familial_hypercholesterolemia)_mrna,

m57892mrna_775-1267,carbonic_anhydrase_isozyme_vi_(ca6)_mrna,_complete_cds_

u09303_2354-2870,t_cell_leukemia_lerk-2_(eplg2)_mrna,_complete_cds_

5 v00594mrna_15-316,mrna_for_metallothionein_from_cadmium-

treated_cells,mrna_for_metallothionein_from_

x59871mrna_2672-2836,tcf-1_mrna_for_t_cell_factor(splice_form_c)

z47556mrna#2_1596-

1866,_semenogelin_ii_gene_extracted_fromgenes_for_semenogelin_i_and_semenogelin_ii

10

Metagene 324

d29810_835-1363,mrna_for_unknown_product,_partial_cds

176224_3424-3970,nmda_receptor_mrna,_complete_cds_

15 all_m24349_838-1316,parathyroid_hormone-like_protein_(plp)_gene,_exon_4,_clones_lambda-plpg(1,3,7-2)

s81944_1173-1689,_gamma-

aminobutyric_acid_type_a_receptor_alpha_subunit_[human,_cerebellum,_mrna_part

all_u03642_1060-1565,g_protein-coupled_receptor_apj_gene,_complete_cds_

20 all_u06155_512-

660,chromosome_1q_subtelomeric_sequence_d1s553/gb=u06155/_ntype=dna/_annot=cds,chromo

u19557_998-1104,squamous_cell_carcinoma_antigen(scca2)_mrna,_complete_cds_

u32659_1393-1825,il-17_mrna,_complete_cds

u43519_2976-3474,dystrophin-related_protein(drp2)_mrna,_complete_cds

25 u88902_cds1_f_at_u88902_u88902,_40_in_u88902cds#1_19-247:_21_in_reversesequence,_289-

499,_integrase_

x80915mrna_1908-2322,gdf5_gene

y10205mrna_146-548,mrna_for_cd88_protein/gb=y10205/_ntype=rna

30 Metagene 204

d42040_4334-4623,mrna_for_kiaa9001_gene,_complete_cds

u07695_3362-3770,tyrosine_kinase_(htk)_mrna,_complete_cds

u19252_4495-5045,putative_transmembrane_protein_mrna,_complete_cds_

35 u32680_1088-1664,cln3_mrna,_complete_cds_

u80073_1289-1655,tip_associating_protein_(tap)_mrna,_complete_cds/gb=u80073/_ntype=rna_

x06745mrna_4850-5288,mrna_for_dna_polymerase_alpha-subunit_

all_x52896_1629-2195,rna_for_dermal_fibroblast_elastin_

x53742mrna_1930-2470,mrna_for_fibulin-1_b

x54667cds_110-326,mrna_for_cystatin_s,mrna_for_cystatin_s_
x59303cds_3274-3773,g7a_mrna_for_valyl-tRNA_synthetase_
x64728cds_1694-1946:in_reversesequence,_2140-2278,chm1_mrna
x79440cds_1303-1759:in_reversesequence,_1827-1851,mrna_for_nadp+-dependent_malic_enzyme_
5 all_x97198_5010-5545,mrna_for_receptor_phosphate_pcp-2_
all_x99975_3672-4243,mrna_for_hrtr/hgcnf_protein_
y08612cds_1849-2197:in_reversesequence,_2257-2269,mrna_for_nup88_protein
y10514mrna_6-270,mrna_for_cd152_protein/gb=y10514_ntype=rna_
all_z80788_607-1040,h4/l_gene

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Metagene 101

d13814_960-1532,mrna_for_angiotensin_ii_type_1b_receptor,_complete_cds_
m63175_1221-1689,autocrine_motility_factor_receptor_mrna_
15 u22029_1690-2227,cytochrome_p450_(cyp2a7)_mrna,_complete_cds_
x13930cds_1147-1454:in_reversesequence,_1650-1695,cyp2a4_mrna_for_p-450_iiA4_protein
x63187mrna_91-511,he4_mrna_for_extracellular_proteinase_inhibitor_homologue

Metagene 177

20

hg1148-ht1148_at_hg1148-ht1148_lipopolysaccharide-binding_protein
hg2309-ht2405_at_hg2309-ht2405_insulin-like_growth_factor_ib_
u70370_1511-2012,hindlimb_expressed_homeobox_protein_backfoot_(bft)_mrna,_complete_cds_
all_x15573_2313-2800,liver-type_1-phosphofructokinase_(pfkl)_mrna,_complete_cds
25 x66365cds_543-957:in_reversesequence,_1080-
1206,mrna_plstire_for_serine/threonine_protein_kinase
all_x85786_1751-2262,mrna_for_dna_binding_regulatory_factor
x86564cds_417-446:not_in_gb_record,fhr-2_gene,_exon_1_
all_x95240_1487-2056,mrna_for_cysteine-rich_secretory_protein-3

30

Metagene 52

hg2841-ht2969_s_at_hg2841-ht2969_albumin,_altslice_3,_missplicing_in_alloalbumin_venezia
hg3417-ht3600_s_at_hg3417-ht3600_gtp_cyclohydrolase_i,_altslice_1_
35 j05008exon#5_637-1183,endothelin-1_(edn1)_gene,_complete_cds
u44105_314-574,rab9_expressed_pseudogene_mrna,_complete_cds
all_x04602_920-1086,mrna_for_interleukin_bsF-2_(b-cell_differentiation_factor)_

Metagene 93

d85423_133-439,mrna_for_cdc5,_partial_cds/gb=d85423/_ntype=rna_
 u23070_938-1460,putative_transmembrane_protein_(nma)_mrna,_complete_cds
 all_x52001_1770-2281,endothelinmrna_
 5 x83863cds_1151-1241,mrna_for_prostaglandin_e_receptor_(ep3f)_
 z34822_f_at_z34822_z34822_4040_in_z34822_6145-6595,(hlcc85)_mrna_for_voltage-
 dependent_l-type_ca_ch

Metagene 421

10

hg3255-ht3432_at_hg3255-ht3432_gamma-aminobutyric_acid_(gaba)_a_receptor_betasubunit
 hg4108-ht4378_at_hg4108-ht4378_olfactory_receptor_or17-24
 m22490_1282-1630,bone_morphogenetic_protein-2b_(bmp-2b)_mrna_
 m95925_1366-1852,leucine_zipper_on_the_d14s46e_locus_mrna,_complete_cds
 15 u27333_2523-
 2728,alpha_(1,3)_fucosyltransferase_(fut6)_mrna,_major_transcript_i,_complete_cds, alpha_
 u35735_2115-2442,rach1_(rach1)_mrna,_complete_cds
 u44799_299-860,u1-snrrnp_binding_protein_homolog_mrna,_complete_cds_

20

Metagene 371
 d86096_cds6_at_d86096_d86096,not_in_gb_record,_ep3-
 iv_gene_extracted_fromdna_for_prostaglandin_e_rec
 s62907_1577-2136,_gamma-

25

aminobutyric_acida_receptor_alpha_subunit_[human,_fetal_brain,_mrna,_2189_nt]
 u33920_2564-2644,clone_lambdasemaphorin_mrna,_complete_cds
 u87309_4315-4843,hvps41p_(hvps41)_mrna,_complete_cds_
 u96114_2964-3390,nedd-4-like_ubiquitin-protein_ligase_pp2_mrna,_complete_cds.
 all_x82018_2942-3459,mrna_for_zid_protein

30

Metagene 306

hg3238-ht4861_s_at_hg3238-ht4861_prostaglandin_ep3_receptor,_altslice_8_
 s72904_1884-
 35 2322,_apk1_antigen=mab_ki_recognized_[human,_ovarian_carcinoma_cell_line_ovcar-3,_mrna,_
 u45285_2099-2579,specific_116-kda_vacuolar_proton_pump_subunit_(oc-
 116kda)_mrna,_complete_cds
 u80017mrna#1_412-
 673,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcription

x01057mrna_1492-1738,mrna_for_interleukin-2_receptor_
 x95592_558-1122,mrna_for_c1d_protein_
 x97301mrna_13-148,mrna_for_ptg-11_protein/gb=x97301_/ntype=rna_

5 Metagene 479

ab002318_6384-6786,mrna_for_kiaa0320_gene,_partial_cds/gb=ab002318_/ntype=rna
 ac000099_12194-12426:in_ac000099cds_519-556:in_all_ac000099_12207,_cosmid_g0771a003_
 af010193_2552-3044,mad-related_gene_smad7_(smad7)_mrna,_complete_cds
10 d13634_1915-2419,mrna_for_kiaa0009_gene,_complete_cds
 d17516_1075-1615,mrna_for_pacap_receptor,_complete_cds_
 d61391_1169-1685,mrna_for_phosphoribosypyrophosphate_synthetase-
 associated_protein_39,_complete_cds
 d78011_1552-2098,mrna_for_dihydropyrimidinase,_complete_cds
15 d83920_732-1158,uterus_mrna_forficolin-1,_complete_cds
 hg1723-ht1729_at_hg1723-ht1729_macrophage_scavenger_receptor,_altslice_2
 hg315-ht315_at_hg315-ht315_beta-1-glycoprotein_11,_pregnancy-specific
 hg3242-ht3419_s_at_hg3242-ht3419_calcium_channel,_voltage-
 gated,_alpha_1e_subunit,_altslice_2_
20 j03798_1026-1536,autoantigen_small_nuclear_ribonucleoprotein_sm-d_mrna,_complete_cds_
 101664_43-529,eosinophil_charcot-
 leyden_crystal_(clc)_protein_(lysophospholipase)_mrna,_complete_cds
 103411_798-1260,rd_protein_(rd)_mrna,_complete_cds_
 all_105512_1285-1313:not_in_gb_record,histatin(his1)_gene
25 l25441_1410-1890,geranylgeranyltransferase_type_i_beta-subunit_mrna,_complete_cds
 l26081_1959-2487,semaphorin-iii_(hsema-i)_mrna,_complete_cds
 l38929mrna_5668-6190,protein_tyrosine_phosphatase_delta_mrna,_complete_cds
 140586_1123-1255,iduronate-2-sulphatase_(ids)_mrna,_complete_cds
 l41066_2321-2831,nf-at3_mrna,_complete_cds
30 l76670_502-1071,nkat7_mrna,_complete_cds
 m58297_2215-2653,zinc_finger_protein_42_(mzf-1)_mrna,_complete_cds_
 m91036mrna#1_37-529,_g-gamma_globin_gene_extracted_fromg-gamma_globin_and_a-
 gamma_globin_genes,_comp
 m95724_2549-2939,centromere_autoantigen_c_(cenpc)_mrna,_complete_cds_
35 s78203_2096-2660,_pept_2=h+/peptide_cotransporter_[human,_kidney,_mrna_partial,_2685_nt]
 s83365_109-343,_putative_rab5-interacting_protein_{clone_11-
 94}_{[human,_hela_cells,_mrna_partial,_36
 u07223mrna_1930-2410,beta2-chimaerin_mrna,_complete_cds
 u18932_4216-4756,heparan_sulfate-n-deacetylase/n-sulfotransferase_mrna,_clone_hsst3'_-,_3'_utr

u26032_2176-2596,translation_initiation_factor_eif-2alpha_mrna,_3'_utr_
 u32581_2488-2884,lambda/iota-protein_kinase_c-interacting_protein_mrna,_complete_cds
 u52700_70-328,tenascin-x_(xb)_mrna,_race_clone_n1,_partial_cds/gb=u52700_/ntype=rna
 u62438_1545-1875,nicotinic_acetylcholine_receptor_beta3_subunit_precursor,_mrna,_complete_cds
5 u67932mrna_1128-
 1700,camp_phosphodiesterase_(pde7a2)_mrna,_complete_cds/gb=u67932_/ntype=rna
 u68488_1013-1397,5-hydroxytryptamine7_receptor_isoform_d_mrna,_complete_cds
 u85267_7-
 145,down_syndrome_critical_region(dscr1)_gene,_alternative_exon_1,_partial_cds/gb=u85267_/n
10 all_x16667_1634-1917,hox2g_mrna_from_the_hox2_locus
 all_x74987_2208-2684,mrna_for_2'_-5'_oligoadenylate_binding_protein
 all_x76040_2954-3309,mrna_for_ion_protease-like_protein
 x76498exon#3_63-369:in_reversesequence,_2899-3043,gene_for_uterine_bombesin_receptor
 all_x78520_3490-3935,_hsapiens_rna_for_clcn3
15 all_x81636_2127-2329,clathrin_light_chain_a_gene_
 all_x81637_5805-5938,clathrin_light_chain_b_gene_
 all_x91992_1340-1929,mrna_for_alkb_protein_homolog_
 x93017exon_1293-1797,ncx2_gene_(exon_2)/gb=x93017_/ntype=dna/_annot=exon_
 all_x96753_7313-7896,mrna_for_melanoma-associated_chondroitin_sulfate_proteoglycan_(mcsp)
20 all_y00064_1931-2418,mrna_for_secretogranin_i_(chromogranin_b)_
 y08991cds_3846-4038:in_reversesequence,_4743-4845,mrna_for_adaptor_protein_p150_
 z34897_1138-1654,mrna_for_h1_histamine_receptor

Metagene 239

25
 ab000409_2046-2538,mrna_for_mnk1,_complete_cds_
 af000430_1941-2427,dynamin-like_protein_mrna,_complete_cds
 af009426_7540-8044,clone_22_mrna,_alternative_splice_variant_beta-
 1,_complete_cds/gb=af009426_/ntype
30 d14660_739-1249,mrna_for_kiaa0104_gene,_complete_cds_
 d14878_1001-1499,mrna_for_protein_d123,_complete_cds_
 d38251_642-1149,mrna_for_rpb5_(xap4),_complete_cds_
 d50678_3909-4413,mrna_for_apolipoprotein_e_receptor_2,_complete_cds
 d87448_4763-5183,mrna_for_kiaa0259_gene,_partial_cds_
35 hg1102-ht1102_at_hg1102-ht1102_ras-related_c3_botulinum_toxin_substrate
 hg3400-ht3579_at_hg3400-ht3579_nestin
 hg4120-ht4392_s_at_hg4120-ht4392_protein_kinase_pitslre,_alpha,_altssplice_1-feb
 hg944-ht944_s_at_hg944-ht944_dopamine_receptor_d4
 j03626mrna#1_1151-1653,_umps_gene_extracted_fromump_synthase_mrna,_complete_cds_

102547_1290-1752,(clone_pz50-19)_cleavage_stimulation_factor_50kda_subunit,_complete_cds
 177864_2060-2618,stat-like_protein_(fe65)_mrna,_complete_cds_
 m29580mrna_1813-2326,zinc-finger_protein(zfp7)_mrna,_complete_cds_
 m81181_2360-2731,sodium/potassium_atpase_beta-2_subunit_(atpb2)_mrna,_complete_cds_
 5 s81221_2246-2546,_lanosterol_synthase_[human,_fetal_liver,_mrna_partial,_2637_nt]
 u07349_2331-2805,b_lymphocyte_serine/threonine_protein_kinase_mrna,_complete_cds_
 u36221_1562-1814,pancreatic_zymogen_granule_membrane_protein_gp-2_mrna,_complete_cds_
 u36787_491-995,putative_holocytochrome_c-type_synthetase_mrna,_complete_cds
 u38864_1766-2186,zinc-finger_protein_c2h2-150_mrna,_complete_cds_
 10 u40271_3598-3999,transmembrane_receptor_precursor_(ptk7)_mrna,_complete_cds
 u41804_882-1254,putative_t1/st2_receptor_binding_protein_precursor_mrna,_complete_cds
 u51903_5202-5712,rasgap-related_protein_(iqgap2)_mrna,_complete_cds
 u52969_19-505,pep19_(pcp4)_mrna,_complete_cds
 u71207_1846-2224,eyes_absent_homolog_(eab1)_mrna,_complete_cds.
 15 u79256_655-1033,clone_23719_mrna_sequence
 all_v00594_15-75,mrna_for_metallothionein_from_cadmium-treated_cells,mrna_for_metallothionein_from_c
 all_x04434_4484-4971,mrna_for_insulin-like_growth_factor_i_receptor
 x07438exon#2_11-
 20 166,dna_for_cellular_retinol_binding_protein_(crbp)_exonsand/gb=x07438_ntype=dna_a
 x58199mrna_2491-2573,mrna_for_beta_adducin
 all_x72304_1456-1688,mrna_for_corticotrophin_releasing_factor_receptor
 x87344mrna#26_769-945,dna,_dmb,_hla-z1,_ipp2,_lmp2,_tap1,_lmp7,_tap2,_dob,_dqb2_and_ring8,_9, and gene
 25 all_z14093_1190-1743,mrna_for_branched_chain_decarboxylase_alpha_subunit_

Metagene 452

30 m38180mrna_1319-1623,3-beta-hydroxysteroid_dehydrogenase/delta-5-delta-4-isomerase_(3-beta-hsd)_gene

Metagene 395

35 hg881-ht881_at_hg881-ht881_mucin_6_gastric
 100190mrna_912-1384,antithrombin_iii_(atiii)_gene,_exonand_complete_cds
 m16973mrna_1406-1910,complement_protein_c8_beta_subunit_mrna,_complete_cds_
 all_m21642_180-
 301,(dysfunctional)_antithrombin_iii_(atiii)_utah_gene,(dysfunctional)_antithrombin_i
 m26682_721-1171,t-cell_translocation_gene(ttg-1)_mrna,_complete_cds_

m54992_924-1494,b_cell_differentiation_antigen_mrna,_complete_cds
 m81883mrna_3226-3538,glutamate_decarboxylase_(gad67)_mrna,_complete_cds
 m83712_1078-1646,nicotinic_receptor_alpha_subunit_mrna,_complete_cds.
 s75174_1316-1511,_e2f-4=transcription_factor_[human,_nalm6_and_hela_cells,_mrna,_1539_nt]
5 u16129_2108-2684,glutamate_receptor_(glur4)_mrna,_complete_cds.
 u50360_81-385,calcium,_calmodulin-dependent_protein_kinase_ii_gamma_mrna,_partial_cds/gb=u50360_/nty
 u79248_1157-1553,clone_23826_mrna_sequence_
 x51698cds_39-343:in_reversesequence_,_387-465,spasmolytic_polypeptide_(sp)_mrna
10 all_x72925_3671-4008,mrna_for_desmocollin_type_1_
 x90828exon#2_233-752,mrna_for_transcription_factor,_lbx1_
 y11180mrna_31-247,mrna_for_twist_protein,_partial/gb=y11180_/ntype=rna_

Metagene 84

15
 d28589mrna_281-743,mrna_(kiaa00167),_partial_sequence/gb=d28589_/ntype=rna_
 d79991_5181-5613,mrna_for_kiaa0169_gene,_partial_cds_
 l11573_1101-1665,surfactant_protein_b_mrna,_complete_cds/gb=l11573_/ntype=rna
 u79528_1038-1577,sr31747_binding_proteinmrna,_complete_cds

20

Metagene 5

m20030_68-612,small_proline_rich_protein_(sprii)_mrna,_clone_930_

25 Metagene 164

af009674_2870-3308,axin_(axin)_mrna,_partial_cds
 d13748_812-1352,mrna_for_eukaryotic_initiation_factor_4ai
 d16562_514-1042,mrna_for_atp_synthase_gamma-subunit_(l-type),_complete_cds_
30 d28473_3882-4418,t-lymphocyte_mrna_for_isoleucyl-trna_synthetase,_complete_cds_
 d29643_1079-1469,mrna_for_kiaa0115_gene,_complete_cds
 d32050_2761-3307,mrna_for_alanyl-trna_synthetase,_complete_cds_
 d42073_1551-2049,mrna_for_reticulocalbin,_complete_cds_
 d50063_1139-1553,mrna_for_proteasome_subunit_p40/_mov34_protein,_complete_cds_
35 d63478_2816-3308,mrna_for_kiaa0144_gene,_complete_cds
 d80000_5250-5754,mrna_for_kiaa0178_gene,_partial_cds_
 d86970_5998-6400,mrna_for_kiaa0216_gene,_complete_cds
 d87071_5779-6223,mrna_for_kiaa0233_gene,_complete_cds
 d87437_4613-5039,mrna_for_kiaa0250_gene,_complete_cds

d89052_428-938,mrna_for_proton-atpase-like_protein,_complete_cds_
 hg1153-ht1153_at_hg1153-ht1153_nucleoside_diphosphate_kinase_nm23-h2s
 hg2279-ht2375_at_hg2279-ht2375_triosephosphate_isomerase_
 j03191mrna_192-684,profilin_mrna,_complete_cds_
 5 j04031_2529-3057,methylenetetrahydrofolate_dehydrogenase-
 _methenyltetrahydrofolate_cyclohydrolase-fo
 j04988cds_1925-2147:in_reversesequence,_7591-
 7831,90_kd_heat_shock_protein_gene,_complete_cds_
 110678_1128-1650,profilin_ii_mrna,_complete_cds
 10 l11669_1355-1715,tetracycline_transporter-like_protein_mrna,_complete_cds
 114076_1469-2051,pre-mrna_splicing_factor_srp75_mrna,_complete_cds_
 116842_1402-1792,ubiquinol_cytochrome-c_reductase_core_i_protein_mrna,_complete_cds
 l20010_7717-8185,hcf1_gene_related_mrna_sequence_
 l33243mrna_13655-14051,polycystic_kidney_diseaseprotein_(pkd1)_mrna,_complete_cds
 15 l38696_961-1375,autoantigen_p542_mrna,_3'_end_of_cds
 m11433_115-403,cellular_retinol-binding_protein_mrna,_complete_cds_
 m31606mrna_1102-1528,phosphorylase_kinase_(psk-c3)_mrna,_complete_cds
 all_m34677_1486-1913,nested_gene_protein_gene,_complete_cds
 m57567_491-953,adp-ribosylation_factor_(harf5)_mrna,_complete_cds
 20 m61832_1472-2002,s-adenosylhomocysteine_hydrolase_(ahcy)_mrna,_complete_cds
 m81601_2039-2483,transcription_elongation_factor_(sii)_mrna,_complete_cds
 m86400_2239-2743,phospholipase_a2_mrna,_complete_cds_
 m88458_585-1095,elp-1_mrna_sequence
 m94362_3717-4179,lamin_b2_(lamb2)_mrna,_partial_cds
 25 m97856_2016-2430,histone-binding_protein_mrna,_complete_cds_
 s75463_1145-
 1565,_p43=mitochondrial_elongation_factor_homolog_[human,_liver,_mrna,_1644_nt]_
 all_u02493_2130-2485,54_kda_protein_mrna,_complete_cds_
 u02619_6437-6965,tfiic_box_b-binding_subunit_mrna,_complete_cds_
 30 u18321_1065-1569,ionizing_radiation_resistance_conferring_protein_mrna,_complete_cds_
 u20285_1283-1811,gps1_(gps1)_mrna,_complete_cds
 u25988_680-720,pregnancy-specific_glycoprotein(psg13')_mrna,_complete_cds_
 u28386_1405-1933,nuclear_localization_sequence_receptor_hsrp1alpha_mrna,_complete_cds
 u31556_1445-1679,transcription_factor_e2f-5_mrna,_complete_cds_
 35 u33053_2381-2879,lipid-activated_protein_kinase_prk1_mrna,_complete_cds
 u36764_721-997,tgf-beta_receptor_interacting_proteinmrna,_complete_cds
 u39400_1407-1887,nof1_mrna,_complete_cds_
 u47077_13025-13463,dna-dependent_protein_kinase_catalytic_subunit_(dna-
 pkcs)_mrna,_complete_cds

u51586_1262-1676,siah_binding_protein(siahbp1)_mrna,_partial_cds
 u62136_660-1050,putative_enterocyte_differentiation_promoting_factor_mrna,_partial_cds_
 u66711mrna_556-1102,ly-6-related_protein_-9804_gene,_complete_cds_
 u73379_193-661,cyclin-selective_ubiquitin_carrier_protein_mrna,_complete_cds_
 5 u81375_1669-2119,placental_equilibrative_nucleoside_transporter(hent1)_mrna,_complete_cds_
 v00599mrna_903-1380,mrna_fragment_encoding_beta-tubulin(from_clone_d-beta-1)_
 all_x02152_1090-1625,mrna_for_lactate_dehydrogenase-a_(ldh-a,_ec_1.1.1.27)_
 all_x04366_2448-
 2986,mrna_for_calcium_activated_neutral_protease_large_subunit_(mucanp,_calpain,_ec_
 10 all_x05130_1362-1876,mrna_for_prolyl_4-hydroxylase_beta_subunit_(ec_1.14.11.2)_(procollagen-l-
 proline
 all_x14850_1122-1555,h2a.x_mrna_encoding_histone_h2a.x_
 all_x52142_2163-2734,mrna_for_ctp_synthetase_(ec_6.3.4.2)
 x58079mrna_43-565,mrna_for_s100_alpha_protein
 15 x67951cds_312-576:in_reversesequence,_642-888,mrna_for_proliferation-associated_gene_(pag)_
 all_x75208_3276-3781,hek2_mrna_for_protein_tyrosine_kinase_receptor
 all_x97335_3247-3704,mrna_for_kinase_a_anchor_protein
 y10807_650-1227,mrna_for_arginine_methyltransferase,_splice_variant,_1262_bp_
 z27113cds_73-325:in_reversesequence,_439-463,gene_for_rna_polymerase_ii_subunit_14.4_kd_
 20 z48501cds_957-1429,mrna_for_polyadenylate_binding_protein_ii/gb=z48501_/ntype=rna
 z48950exon#4_794-1100,hh3.3b_gene_for_histone_h3.3_

Metagene 136

25 ac000064cds#2_102-372:in_fullsequence,_6375-
 6621,_wugsc:h_rg083m05.2_gene_extracted_frombac_clone_rg
 ac000064cds#1_1287-1581:in_reversesequence,_16950-
 17160,_wugsc:h_rg083m05.2_gene_extracted_frombac_c
 af000177_293-851,sm-like_protein_casm_(casm)_mrna,_complete_cds/gb=af000177_/ntype=rna
 30 af000231_1768-2308,rab11a_gtpase_mrna,_complete_cds.
 af015950_3501-3909,telomerase_reverse_transcriptase_(hrt)_mrna,_complete_cds.
 d10656_988-1528,mrna_for_crk-ii,_complete_cds
 d63391_341-773,mrna_for_platelet_activating_factor_acetylhydrolase_ib_gamma-
 subunit,_complete_cds
 35 d86959_5435-5867,mrna_for_kiaa0204_gene,_complete_cds
 hg3104-ht3280_at_hg3104-ht3280_serine_protease_met1
 134820_566-938,nad+-dependent_succinate-semialdehyde_dehydrogenase_(ssadh)_mrna,_3'_end
 m37400mrna_1352-1886,cytosolic_aspartate_aminotransferase_mrna,_complete_cds_
 m63483_757-1255,major_nuclear_matrix_protein_mrna

m68891_2398-2686,gata-binding_protein_(gata2)_mrna,_complete_cds_
 s72370_3422-3962,_pyruvate_carboxylase_[human,_kidney,_mrna,_4017_nt]_
 u01160_1056-1635,transmembranesuperfamily_protein_(sas)_mrna,_complete_cds
 u39412_675-1209:not_in_gb_record,platelet_alpha_snap_mrna,_complete_cds
5 u44755_965-1487,pse-binding_factor_ptf_delta_subunit_mrna,_complete_cds
 u44839_2566-3088,putative_ubiquitin_c-terminal_hydrolase_(uhx1)_mrna,_complete_cds_
 u66469_819-1209,cell_growth_regulator_cgr19_mrna,_complete_cds_
 u87972_91-373,nad+-isocitrate_dehydrogenase_mrna,_partial_cds/gb=u87972_/ntype=rna_
 all_x12433_1247-1734,phs1-2_mrna_with_orf_homologous_to_membrane_receptor_proteins
10 all_x17025_1254-1807,homolog_of_yeast_ipp_isomerase

Metagene 262

d90070_1329-1828,atl-derived_pma-responsive_(apr)_peptide_mrna_
15 m69181_6995-7523,nonmuscle_myosin_heavy_chain-b_(myh10)_mrna,_partial_cds
 u02680_2435-2837,protein_tyrosine_kinase_mrna,_complete_cds

Metagene 391

20 176627mrna_5831-
 6329,metabotropic_glutamate_receptoralpha_(mglur1alpha)_mrna,_complete_cds_
 m55422_2463-2733,krueppel-related_zinc_finger_protein_(h-plk)_mrna,_complete_cds_
 all_m61855_1535-1714,cytochrome_p4502c9_(cyp2c9)_mrna,_clone_25
 all_x14968_1221-1636,testis_mrna_for_the_rii-alpha_subunit_of_camp_dependent_protein_kinase
25 x61079mrna_10-211,mrna_for_t_cell_receptor,_clone_igra24.
 z16411cds_2917-3110:in_reversesequence_,3137-3441,mrna_encoding_phospholipase_c

Metagene 276

30 hg1067-ht1067_r_at_hg1067-ht1067_mucin_
 u43292_706-1252,mds1b_(mds1)_mrna,_complete_cds
 all_x83492_418-500,mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(4,7))/gb=x83492_/ntype=rna,mrna_for_fa
 x95826cds_203-773,art4_gene/gb=x95826_/ntype=dna/_annot=cds
35 x99894_936-1482,mrna_coding_for_insulin_promoter_factor_1

Metagene 76

d50310_731-1127,mrna_for_cyclin_i,_complete_cds

d87735_127-643,mrna_for_ribosomal_protein_114,_complete_cds
hg1515-hg1515_f_at_hg1515-hg1515_transcription_factor_btf3b
hg3117-hg3293_at_hg3117-hg3293_mps1
hg384-hg384_at_hg384-hg384_ribosomal_protein_126_

5 hg429-hg429_at_hg429-hg429_b-cell_growth_factor_
hg613-hg613_at_hg613-hg613_ribosomal_protein_s12_
hg688-hg688_f_at_hg688-hg688_major_histocompatibility_complex_ii_dr_beta_2_
j03459mrna_1459-1855,leukotriene_a-4_hydrolase_mrna,_complete_cds
10 108666_953-1421,porin_(por)_mrna,_complete_cds_and_truncated_cds
l36870mrna_3077-3533,map_kinase_kinase(mkk4)_mrna,_complete_cds
m13934cds#2_41-407:in_reversesequence,_5551-
5557,_rps14_gene_(unknown_protein)_extracted_fromribosom
m14199_2-381,laminin_receptor_(2h5_epitope)_mrna,_5'_end_
m17885mrna_532-946,acidic_ribosomal_phosphoprotein_p0_mrna,_complete_cds_

15 m26730cds_3-273:in_reversesequence,_99-204,mitochondrial_ubiquinone-
binding_protein_gene,_5'_flank_w
m75126_3159-3537,hexokinase(hk1)_mrna,_complete_cds_
m84711_345-831,v-fos_transformation_effector_protein_(fte-1),_mrna_complete_cds
u12404_111-651,csa-19_mrna,_complete_cds_

20 u14970_122-656,ribosomal_protein_s5_mrna,_complete_cds_
u14972_103-499,ribosomal_protein_s10_mrna,_complete_cds
u21049cds_61-319:in_reversesequence,_592-760,dd96_mrna,_complete_cds
u58682_31-313,ribosomal_protein_s28_mrna,_complete_cds_
u65092_324-774,melanocyte-specific_gene(msg1)_mrna,_complete_cds

25 u70323_3897-4401,ataxin-2_(sca2)_mrna,_complete_cds
u70439_956-1407,silver-stainable_protein_ssp29_mrna,_complete_cds
v01516cds_713-1044:in_reversesequence,_1070-
1293,messenger_fragment_encoding_cytoskeletal_keratin_(t
all_x04347_618-917,liver_mrna_fragment_dna_binding_protein_upi_homologue_(c-terminus)

30 x12671mrna_1450-
1726,_hnrrnp_a1_protein_gene_extracted_fromgene_for_heterogeneous_nuclear_ribonucleop
x15940cds_66-348:in_reversesequence,_379-385,mrna_for_ribosomal_protein_131_
x16560cds_1-163:in_reversesequence,_13-
295,cox_viiic_gene_for_subunit_viiic_of_cytochrome_c_oxidase_(e

35 x53777cds_81-435,l23_mrna_for_putative_ribosomal_protein_
x55733cds_1611-1773:in_reversesequence,_1840-2056,initiation_factor_4b_cdna
x55954cds_19-385:in_reversesequence,_427-433,mrna_for_hl23_ribosomal_protein_homologue
x62691cds_13-343,mrna_for_ribosomal_protein_(homologous_to_yeast_s24)_
x73460cds_725-1133:in_reversesequence,_1211,mrna_for_ribosomal_protein_13_

x76013cds_1933-2257:in_reversesequence,_2328-2394,qrshs_mrna_for_glutaminyl-tRNA_synthetase_
x80822cds_13-331:in_reversesequence,_56-578,mrna_for_orf
x80909cds_297-591:in_reversesequence,_694-754,alpha_nac_mrna
all_y00339_913-1465,mrna_for_carbonic_anhydrase_ii_(ec_4.2.1.1)
5 y08915_749-1235,mrna_for_alpha_protein_

Metagene 130

ab002315_4819-5347,mrna_for_kiaa0317_gene,_complete_cds/gb=ab002315/_ntype=rna
10 ab002382_4858-5320,mrna_for_kiaa0384_gene,_complete_cds/gb=ab002382/_ntype=rna_ac002115mrna#2_3349-
7559:not_in_gb_record,_cox6b_gene_(coxg)_extracted_from_dna_from_overlapping_chro
af002020_4090-4600,niemann-
pick_c_disease_protein_(npc1)_mrna,_complete_cds/gb=af002020/_ntype=rna
15 d14657_355-775,mrna_for_kiaa0101_gene,_complete_cds
d25248_4510-5050,randomly_sequenced_mrna_

d25304_4431-4701,mrna_for_kiaa0006_gene,_partial_cds_

d25547_779-864,mrna_for_pimt_isozyme_i,_complete_cds_

d28476_5899-6385,mrna_for_kiaa0045_gene,_complete_cds_

20 d55716_1952-2378,mrna_for_p1cdc47,_complete_cds
d63876_3171-3717,mrna_for_kiaa0154_gene,_partial_cds_

d79998_3100-3562,mrna_for_kiaa0176_gene,_partial_cds_

d83004_644-1148,epidermoid_carcinoma_mrna_for_ubiquitin-
conjugating_enzyme_e2_similar_to_drosophila_

25 d83785_5214-5634,mrna_for_kiaa0200_gene,_complete_cds
d85181_1502-2018,mrna_for_fungal_sterol-c5-desaturase_homolog,_complete_cds
d86550_5888-6338,mrna_for_serine/threonine_protein_kinase,_complete_cds
d87451_2622-3162,mrna_for_kiaa0262_gene,_complete_cds
d87969_1206-1686,mrna_for_cmp-sialic_acid_transporter,_complete_cds
30 hg2492-ht2588_at_hg2492-ht2588 glutamate_receptor_subunit
hg4557-ht4962_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_1snrp_

l07758_1288-1762,ief_ssp_9502_mrna,_complete_cds_

113738mrna_4076-4490,activated_p21cdc42hs_kinase_(ack)_mrna,_complete_cds
all_119314_3362-3789,hry_gene,_complete_cds_

35 l20859_2655-3159,leukemia_virus_receptor(glvr1)_mrna,_complete_cds
l21936_1796-2222,succinate_dehydrogenase_flavoprotein_subunit_(sdh)_mrna,_complete_cds_

l27706_1445-1985,chaperonin_protein_(tcp20)_gene_complete_cds_

l34600_1958-2426,nuclear-encoded_mitochondrial_initiation_factor_mrna,_complete_cds_

all_m22877_1917-2434,somatic_cytochrome_c_(hcs)_gene,_complete_cds_

m29960mrna_1721-2141,steroid_receptor_(tr2-11)_mrna,_complete_cds
m31932mrna_1771-2341,igg_low_affinity_fc_fragment_receptor_(fcrlia)_mrna,_complete_cds_
m32011mrna_1623-2157,neutrophil_oxidase_factor_(p67-phox)_mrna,_complete_cds_
m33336_2441-3005,camp-dependent_protein_kinase_type_i-
5 alpha_subunit_(prkar1a)_mrna,_complete_cds_
m75715_1635-2185,tb3-1_mrna,_complete_cds
u07559_1832-2366,isl-1_(islet-1)_mrna,_complete_cds
u11872_36-72,interleukin-
8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb1,_partial_cds/gb=u1187
10 u15642_975-1472,transcription_factor_e2f-5_mrna,_complete_cds
u47927_2598-3132,isopeptidase_t_(isot)_mrna,_complete_cds
u48296_1629-2175,protein_tyrosine_phosphatase_ptpcaax1_(hptpcaax1)_mrna,_complete_cds
u52154_2352-2610,g_protein-
coupled_inwardly_rectifying_potassium_channel_kir3.4_mrna,_complete_cds_
15 u63541mrna_431-977,mrna_expressed_in_hc/hcc_livers_and_molt-
4_proliferating_cells,_partial_sequence
u77456_2006-2414,nucleosome_assembly_proteinmrna,_complete_cds
u84720_1431-1611,mrna_export_protein_rae1_(rae1)_mrna,_complete_cds
u89336exon#34-35_35-
20 87:not_in_gb_record,_unknown_gene_extracted_fromhla_iii_regionContaining_notch4
u94832_2732-2958,kh_type_splicing_regulatory_protein_ksrp_mrna,_complete_cds.
u94836_3450-3894,erprot_213-21_mrna,_complete_cds
all_x06272_2379-2854,mrna_for_docking_protein_(signal_recognition_particle_receptor)_
all_x17567_432-1018,rna_for_snrrnp_protein_b
25 all_x63741_3695-4230,pilot_mrna
x66113cds_2199-2633:in_reversesequence,_2682-2729,mrna_for_pm/scl_100kd_nucleolar_protein_
all_x67155_2735-3228,mrna_for_mitotic_kinesin-like_protein-1_ .
all_x79888_965-1500,auh_mrna_
x87613cds_1996-2236:in_reversesequence,_2780-
30 2912,mrna_for_skeletal_muscle_abundant_protein_
all_x95632_1680-1784,mrna_for_arg_protein_tyrosine_kinase-binding_protein
y07707_1136-1634,mrna_for_itba4_gene/gb=y07707_ntype=rna
z84721cds#1_81-390:in_reversesequence,_15248-
15488,dna_sequence_from_cosmid_gg1_from_a_contig_from_t
35 reverse_z86000_20444-20634,dna_sequence_from_pac_151b14_on_chromosome_22q12-
qter_contains_somatostat

ab000462_6801-7227,mrna_for_sh3_binding_protein,_clone_res4-23a,_complete_cds
 m65062_1233-1527,insulin-like_growth_factor_binding_protein(igfbp-5)_mrna,_complete_cds_
 m93221mrna_4618-5110,macrophage_mannose_receptor_(mrc1)_gene_
 u25801_225-675,tax1_binding_protein_mrna,_partial_cds
5 all_x16699_2053-2130,mrna_for_cytochrome_p-450hp_
 x72177mrna_2964-3510,c6_gene,_exon_1

Metagene 427

10 m60459_1277-1745,erythropoietin_receptor_mrna,_complete_cds
 u45880_1969-2515,x-linked_inhibitor_of_apoptosis_protein_xiap_mrna,_complete_cds
 u89326_1533-1965,bone_morphogenetic_protein_receptor_type_i_alk-6_mrna,_complete_cds_
 all_x66610_1372-1697,mrna_for_enolase
 all_x78678_1384-1871,khk_mrna_for_ketohexokinase,_clone_phkhk3a

15

Metagene 230

all_d29675_1092-
 1149,inducible_nitric_oxide_synthase_gene,_promoter_and_exon/gb=d29675_/ntype=dna/_a
20 d29675exon_2-
 136,inducible_nitric_oxide_synthase_gene,_promoter_and_exon/gb=d29675_/ntype=dna/_annot
 hg2730-ht2827_s_at_hg2730-ht2827_fibrinogen,_a_alpha_polypeptide,_alsplice_2,_e_
 117128_1940-2480,(clone_h4/h16)_gamma-glutamic_carboxylase_mrna,_complete_cds_
 all_m10943_444-1929,metallothionein-if_gene_(hmt-if)
25 m18731_at_m18731_m18731,not_in_gb_record,galactose-1-
 phosphate_uridyltransferase_(galt)_mrna,_comple
 m81933_1920-2394,cdc25a_mrna,_complete_cds_
 s79862_1641-
 2226,_26_s_protease_subunit_5b=50_kda_subunit_[human,_hela_cells,_mrna_partial,_2253_nt]
30 u20734cds_709-1014:in_reversesequence,_7020-
 7258,transcription_factor_junb_(junb)_gene,_5'_region_an
 u43328_1158-1698,link_protein_mrna,_complete_cds_
 u52155_1646-2168,atp-
 dependent_inwardly_rectifying_potassium_channel_kir4.1_mrna,_complete_cds_
35 u77664_417-891,rnasep_protein_p38_(rpp38)_mrna,_complete_cds.
 all_x79483_1063-1556,erk6_mrna_for_extracellular_signal_regulated_kinase_
 y07829exon#2_13-
 364,_exon_fromgene_encoding_ring_finger_protein/gb=y07829_/ntype=dna/_annot=exon,_ex
 all_y08765_1854-2207,mrna_for_splicing_factor,_sf1-hl1_isoform_

Metagene 201

reverse_ac000063_31010-31140,cosmid_clone_luca19_from_3p21.3_

5 hg1761-ht1778_s_at_hg1761-ht1778_tyrosine_kinase_fer_

hg2149-ht2219_at_hg2149-ht2219_mucin_

110338_953-1360,sodium_channel_beta-1_subunit_(scn1b)_mrna,_complete_cds_

120860_2219-2684,glycoprotein_ib_beta_mrna,_complete_cds_

m11186exon#3_20-134:not_in_gb_record,prepro-oxytocin-

10 neurophysin_i_(oxt)_gene,_complete_cds_

m29273_1749-2307,myelin-associated_glycoprotein_(mag)_mrna,_complete_cds_

m55040mrna_1689-2187,acetylcholinesterase_(ache)_mrna,_complete_cds

m64082_1605-2055,flavin-containing_monomooxygenase_(fmo1)_mrna,_complete_cds_

m73481mrna_1227-1641,gastrin_releasing_peptide_receptor_(grpr)_mrna,_complete_cds

15 m76446_1521-1977,alpha-a1-adrenergic_receptor_mrna,_complete_cds_

m86546_1284-1716,pbx1a_and_pbx1b_mrna,_complete_cds

m88282mrna_4784-5180,tactile_protein_mrna,_complete_cds

s75578_755-1286,_4-

aminobutyrate_aminotransferase_[human,_neuroblastoma_be_cells,_mrna_partial,_1352

20 u18991_2113-2638,retinal_pigment_epithelium-

specific_61_kda_protein_(rpe65)_mrna,_complete_cds_

u37251_1908-2328,krab_zinc_finger_protein_(znf177)_mrna,_splicing_variant,_complete_cds

u38268cds_61-379,cytochrome_b_pseudogene,_partial_cds/gb=u38268_ntype=dna_annot=cds

u40990_2251-2797,voltage_gated_potassium_channel_(kv1qt1)_mrna,_complete_cds

25 u70663_1532-1928,zinc_finger_transcription_factor_hezf_(ezf)_mrna,_complete_cds

u78190mrna_159-687,gtp_cyclohydrolase_i_feedback_regulatory_protein_gene,_complete_cds

all_x00237_613-824,f_variable_segment_5'_to_antithrombin_iii_gene_(at_iii)_

x07495cds_389-764:in_reversesequence,_1383-1449,mrna_for_cp19_homeobox_from_hox-3_locus.

all_x51408_1626-2017,mrna_for_n-chimaerin

30 all_x75308_2091-2608,mrna_for_collagenase_3

x80062cds_1187-1268:in_reversesequence,_1430-1463,sa_mrna_

Metagene 190

35 126584_3368-3933,(cdc25)_mrna,_complete_cds

s75168mrna_1515-2079,_matk=megakaryocyte-

associated_tyrosine_kinase_[human,_genomic,_2617_ntsegments

u02609_1934-2450,transducin-like_protein_mrna,_complete_cds

u07882_1382-1730,delta opioid_receptor_mrna,_complete_cds

u16307_996-1458,glioma_pathogenesis-related_protein_(glipr)_mrna,_complete_cds_
 u59831mrna_1876-2385,transcription_factor,_forkhead_related_activator(freac-
 4)_gene,_complete_cds
 y10313_1352-1730:not_in_gb_record,mrna_for_nerve_growth_factor-inducible_pc4_homologue
5 all_z83741_654-1183,hh2a/m_gene

Metagene 69

d85759_2398-2701,fetuses,_20-26_weeks_brain_mrna_for_mnb_protein_kinase,_complete_cds
10 hg2479-ht2575_s_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
 176528exon_146-615,presenilin(ps1;_s182)_gene
 m29551_2520-3054,calcineurin_a2_mrna,_complete_cds
 m83941_2764-3124,receptor_tyrosine_kinase_(hek)_mrna,_complete_cds
 s77154_1862-2362,_tinur=_ngfi-b/nur77_beta-
15 type_transcription_factor_homolog_[human,_t_lymphoid_cell
 u17989_3352-3796,nuclear_autoantigen_gs2na_mrna,_complete_cds
 u56244_at_u56244_u56244,not_in_gb_record,hig-1_mrna,_complete_cds
 u58091_427-883,hs-cul-4b_mrna,_partial_cds
 u69611_2905-2985,tnf-alpha_converting_enzyme_mrna,_complete_cds
20 u72648cds_1037-1354:in_reversesequence,_4177-4210,alpha2-c4-
 adrenergic_receptor_gene,_complete_cds
 u80456_3416-3788,transcription_factor_sim2_long_form_mrna,_complete_cds
 u86755_2390-2735,tnf-alpha_converting_enzyme_mrna,_complete_cds
 all_x79204_10002-10585,scal1_mrna_for_ataxin
25 x83573_1377-1803,arse_mrna_
 x84194cds_61-271:in_reversesequence,_501-
 555,mrna_for_acylphosphatase,_erythrocyte_(ct)_isoenzyme_
 x91196mrna#2_3588-4161,mrna_for_e14_and_a-t_proteins/gb=x91196/_ntype=rna

30 Metagene 178.

ab000895_25-385,mrna_for_cadherin_fib1,_partial_cds/gb=ab000895/_ntype=rna
 all_d00408_1838-1946,fetal_liver_cytochrome_p-450_(p-
 450_hfla),_complete_cds,fetal_liver_cytochrome_
35 d26018_2865-3381,mrna_for_kiaa0039_gene,_partial_cds
 d83646_1984-2452,mrna_for_metalloproteinase,_complete_cds
 d83767_917-1319,clone_n9_rep-8_mrna,_complete_cds
 d84307_1321-1813,cdna_for_phosphoethanolamine_cytidylyltransferase,_complete_cds
 hg2714-ht2810_at_hg2714-ht2810_tyrosine_kinase_

hg3893-ht4163_at_hg3893-ht4163_phosphoglucomutase_1,_altslice_
 112701cds_103-283:in_reversesequence,_325-463,engrailed_protein_(en2)_gene,_5'_end_
 l37882_1340-1814,frizzled_gene_product_mrna,_complete_cds
 141919mrna_1877-2450,hic-1_gene_fragment
5 176937mrna_4642-
 5098,_unnamed_protein_product_gene_extracted_fromwerner_syndrome_gene,_complete_cds
 all_m32053_2900-3489,h19_rna_gene,_complete_cds_(spliced_in_silico)
 all_m58569_4044-4260,fibrinogen_alpha-
 subunit_bipartite_transcript,_complete_cds_of_extended_(alpha-
10 m64710cds_64-353:in_reversesequence,_1226-1353,c-type_natriuretic_peptide_gene,_complete_cds
 m77829_737-1269,channel-like_integral_membrane_protein_(chip28)_mrna,_complete_cds
 m81830cds_716-1040:in_reversesequence,_1170-
 1326,somatostatin_receptor_isoform(ssr2)_gene,_complete
 u03399_1649-2147,t-complex_protein_10a_(tcp10a)_mrna,_complete_cds
15 u11287_5386-5932,n-methyl-d-aspartate_receptor_subunit_nr3_(hnR3)_mrna,_complete_cds
 u12622_4-
 358,beaded_intermediate_filament_protein_cp115_mrna,_partial_cds/gb=u12622_ntype=rna
 u22314_2753-3311,rest_protein_mrna,_complete_cds
 u48436_5739-6290,fragile_x_mental_retardation_protein_fmr2p_(fmr2)_mrna,_complete_cds
20 u50315_2179-2551,enhancer_of_zeste_homolog(ezh1)_mrna,_complete_cds
 all_u58658_522-1093,unknown_protein_mrna_within_the_p53_intron_1,_complete_cds
 u62431_2093-
 2633,nicotinic_acetylcholine_receptor_alpha2_subunit_precursor,_mrna,_complete_cds
 u87460_3537-4113,putative_endothelin_receptor_type_b-like_protein_mrna,_complete_cds
25 u89335exon#30_375-
 909,_notch4_gene_(notch4)_extracted_fromhla_iii_region_containing_notch4_(notch4)_
 x62429cds_438-784:in_reversesequence,_877-994,mrna_for_transcription_factor_pit-1_
 all_x75315_849-1348,seb4b_mrna
 x83703mrna_1284-1854,mrna_for_cytokine_inducible_nuclear_protein
30 all_z35102_2543-3018,mrna_for_ndr_protein_kinase
 z48512exon#4_87-303,xg_mrna_(clone_pep6)/gb=z48512_ntype=rna
 all_z83742_507-757,hh2a/c_gene.

35

hg3242-ht4231_s_at_hg3242-ht4231_calcium_channel,_voltage-
 gated,_alpha_1e_subunit,_altslice_3_
 hg4258-ht4528_at_hg4258-ht4528_kinase_inhibitor_p27kip1,_cyclin-dependent
 hg4411-ht4681_at_hg4411-ht4681_mucin,_gastric

hg4677-ht5102_s_at_hg4677-ht5102_oncogene_ret/ptc2,_fusion_activated_
 k01900mrna_655-1213,lymphocyte_interferon_alpha_type_201_mrna,_complete_cds
 132961_1584-1679,4-aminobutyrate_aminotransferase_(gabat)_mrna,_complete_cds_
 178267mrna_2573-3113,par-5_mrna,_probable_5'_end
5 m10612cds_17-275:in_reversesequence,_2926-3822:not_in_gb_record,apolipoprotein_c-
 ii_gene,_complete_c
 m13686_388-897,pulmonary_surfactant-associated_protein_mrna,_complete_cds,_clone_mpsap-6a
 m16591mrna_1446-1933,hemopoietic_cell_protein-
 tyrosine_kinase_(hck)_gene,_complete_cds,_clone_lambda
10 m81829cds_915-1137:in_reversesequence,_1260-
 1476,somatostatin_receptor_isoformgene,_complete_cds_
 s38953cds_611-820:in_reversesequence,_4446-4527,_xa_[human,_genomic,_6873_nt]
 s79281_25-
 463,_pancreatic_ribonuclease_[human,_mrna_recombinant_partial,_491_nt]/gb=s79281_/ntype=rn
15 u25826cds_795-1017:in_reversesequence,_4190-
 4436,transcription_factor_(sc1)_gene,_complete_cds_
 u29725_2517-2937,bmk1_alpha_kinase_mrna,_complete_cds
 u31986_877-1381,cartilage-specific_homeodomain_protein_cart-1_mrna,_complete_cds_
 u36798_4071-4551,platelet_cgi-pde_mrna,_complete_cds
20 u48936_15-139,amiloride-
 sensitive_epithelial_sodium_channel_gamma_subunit_mrna,_5'_end,_partial_cds/
 u49248_4807-
 5251,canalicular_multispecific_organic_anion_transporter_(cmoat),_gene,_complete_cds_
 u49837_684-1218,lim_protein_mlp_mrna,_complete_cds_
25 u53174_1639-2059,cell_cycle_checkpoint_control_protein_mrna,_complete_cds
 u56814_495-957,dnase_i_homologous_protein_(dhp2)_mrna,_complete_cds
 u60062_1060-1550,fez1-t_mrna,_alternatively_spliced_form,_complete_cds_
 u63090_1303-1813,gal_beta-1,3_galnac_alpha-2,3_sialyltransferase_(st3gal_ii)_mrna,_complete_cds
 u79295_817-1345,clone_23961_mrna_sequence
30 all_x65857_1542-2053,hgmp07e_gene_for_olfactory_receptor
 x70070cds_954-1194:in_reversesequence,_1608-1800,mrna_for_neurotensin_receptor
 x77307cds_1244-1382:in_reversesequence,_1491-1701,mrna_for_5-ht2b_serotonin_receptor
 all_x87160_2768-3339,mrna_for_gamma_subunit_of_epithelial_amiloride-
 sensitive_sodium_channel_
35 all_x95095_487-1058,mrna_for_pdgfralpha_protein/gb=x95095_/ntype=mrna
 z26653cds_8896-9286:in_reversesequence,_9383-9509,mrna_for_laminin_m_chain_(merosin)
 all_z37976_6411-6916,mrna_for_latent_transforming_growth_factor-beta_binding_protein_(ltbp-2)
 all_z38133_5578-5993,mrna_for_myosin_
 all_z49825_1747-2253,mrna_for_hepatocyte_nuclear_factoralpha

z70276cds_2-294,mrna_for_fibroblast_growth_factor(partial).
 z83805_199-463,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc8)

Metagene 148

5

d13644_4013-4523,mrna_for_kiaa0019_gene,_complete_cds
 l35545mrna_689-1223,endothelial_cell_protein_c/apc_receptor(epcr)_mrna,_complete_cds_
 m33882_2348-2762,p78_protein_mrna,_complete_cds
 m60750cds_3-348,histone_h2b.1_(h2b)_gene,_complete_cds/gb=m60750_ntype=dna_annot=cds
10
 u78798_1699-2203,tnf_receptor_associated_factor(traf6)_mrna,_complete_cds.
 all_y08319_1743-2272,mrna_for_kinesin-2
 y12556_427-877,mrna_for_amp-activated_protein_kinase_beta-1/gb=y12556_ntype=rna_

Metagene 165

15

af000959_759-1269,transmembrane_protein_mrna,_complete_cds
 d28364_4-
 118,mrna_for_annexin_ii,_5'_utr_(sequence_from_the_5'_cap_to_the_start_codon)/gb=d28364_nt
 hg2239-ht2324_at_hg2239-ht2324_potassium_channel_protein_
20
 hg3075-ht3236_s_at_hg3075-ht3236_focal_adhesion_kinase_
 m28214_255-723,gtp-binding_protein_(rab3b)_mrna,_complete_cds_
 m91368_2656-3189,na+/ca+_exchanger_(cnc)_mrna,_complete_cds
 u79734_4119-4683,huntingtin_interacting_protein_(hip1)_mrna,_complete_cds
 x71345mrna_222-798,mrna_for_trypsinogen_iv_b-form
25
 all_x83535_1791-2208,mrna_for_membrane-type_matrix_metalloproteinase_

Metagene 120

l21998_15275-15677,intestinal_mucin_(muc2)_mrna,_complete_cds
30
 l26234mrna_298-
 796,apolipoprotein_b_mrna_editing_enzyme,_catalytic_polypeptide(apobec1)_mrna,_comple
 m55905_1340-1820,mitochondrial_nad(p)+_dependent_malic_enzyme_mrna,_complete_cds_
 m96956_2590-2639,(clone_cr-3)_teratocarcinoma-
 derived_growth_factor(tdgf3)_mrna,_complete_cds_
35
 u00952_488-998,clone_a9a2brb7_(cac)n/(gtg)n_repeat-containing_mrna_
 u01062mrna_8334-8778,typeinositol_1,4,5-trisphosphate_receptor_(itpr3)_mrna,_complete_cds_
 u17418_1591-2071,parathyroid_hormone/parathyroid_hormone-
 related_peptide_receptor_mrna,_complete_cds
 u31099_13-469,dp_prostanoid_receptor_(ptgdr)_mrna,_partial_cds.

u33838_2-188,nf-kappa-
 b_p65delta3_mrna,_spliced_transcript_lacking_exonsand_7,_partial_cds/gb=u33838
 u40622_999-1449,xrcc4_mrna,_complete_cds_
 u40705_2127-2625,telomeric_repeat_binding_factor_(trf1)_mrna,_complete_cds
5 u66561_2158-2614,kruppel-related_zinc_finger_protein_(znf184)_mrna,_partial_cds
 u90313_212-758,glutathione-s-transferase_homolog_mrna,_complete_cds
 u94333_2877-3429,clq/mbl/spa_receptor_c1qr(p)_mrna,_complete_cds.
 x89576_1772-2255,mrna_for_putative_mt4-mmp_protein_
 z19002cds_1508-1994:in_reversesequence,_2075-2081,of_plzf_gene_encoding_kruppel-
10 like_zinc_finger_pro

Metagene 32

d85376exon_2003-2453,dna_for_thyrotropin-releasing_hormon_receptor_
15 hg1034-ht1034_f_at_hg1034-ht1034_atpase,_na+/k+_transporting,_alphapolypeptide
 hg1471-ht3923_s_at_hg1471-ht3923_transcription_factor_oct-1a/1b,_altslice_2,_oct-1b_
 hg2147-ht2217_r_at_hg2147-ht2217_mucin_3,_intestinal_
 hg3565-ht3768_at_hg3565-ht3768_zinc_finger_protein_
 all_k03431_5910-6163:not_in_gb_record,_hpr_gene_(haptoglobin-
20 related_protein)_extracted_fromhaptoglo
 l03840_2419-2970,fibroblast_growth_factor_receptor(fgfr4)_mrna,_complete_cds
 l07590_4754-5138,protein_phosphatase_2a_130_kda_regulatory_subunit_mrna,_complete_cds
 l11708_761-1205,_humanbeta_hydroxysteroid_dehydrogenase_typemrna,_complete_cds_
 l13197_1853-2099,(clone_d21s418e)_pregnancy-associated_plasma_protein_a_(papp-
25 a)_gene,_5'_utr
 l27943mrna_291-867,cytidine_deaminase_(cda)_mrna,_complete_cds
 l28821_4394-4838,alpha_mannosidase_ii_isozyme_mrna,_complete_cds
 l40992mrna_906-1368,(clone_pebp2aa1)_core-
 binding_factor,_runt_domain,_alpha_subunit(cbfal)_mrna,_3'
30 l49169mrna_3270-3612,g0s3_mrna,_complete_cds
 m14016mrna_644-947,uroporphyrinogen_decarboxylase_mrna,_complete_cds_
 m14660exon_1123-1363:in_reversesequence,_1460-1646,isg-
 54k_gene_(interferon_stimulated_gene)_encodin
 m23892mrna_2101-2549,15-lipoxygenase_mrna,_complete_cds
35 m27288exon_225-555:in_reversesequence,_567-768,oncostatin_m_gene
 m27783_2-433,neutrophil_elastase_mrna,_3'_end
 m28213_94-627,gtp-binding_protein_(rab2)_mrna,_complete_cds_
 m31525mrna_517-1081,mhc_ii_lymphocyte_antigen_(hla-dna)_gene,_complete_cds_
 m55131mrna_5636-6134,cystic_fibrosis_transmembrane_conductance_regulator_(cftr)_gene_

m55172_6712-7102,large_aggregating_cartilage_proteoglycan_core_protein_mrna,_complete_cds
m63896cds_927-1197:in_reversesequence,_1866-
2022,transcriptional_enhancer_factor_(tef1)_dna,_complet
m63967exon#2_1319-1625,mitochondrial_aldehyde_dehydrogenase_x_gene,_complete_cds_

5 m80478exon#3_119-635,platelet_glycoprotein_ix_precursor_(gpix)_gene,_complete_cds
m96995_497-1025,epidermal_growth_factor_receptor-binding_protein_grb2_(egfrbp-
grb2)_mrna_sequence_
s50017cds_904-1241:in_reversesequence,_444-505,_2',3'-cyclic_nucleotide_3'--
phosphodiesterase_[hum

10 u07563_cds1_at_u07563_u07563,not_in_gb_record,abl_gene,_exon_1b_and_intron_1b,_and_putativ
e_m8604_me
u11861_511-949,g10_homolog_(edg-2)_mrna,_complete_cds
u33841_8844-9294,ataxia_telangiectasia_(atm)_mrna,_complete_cds
u34605_3365-3851,retinoic_acid-_and_interferon-inducible_58k_protein_ri58_mrna,_complete_cds_

15 u35246_1518-1962,vacuolar_protein_sorting_homolog_h-vps45_mrna,_complete_cds_
u38980_841-972,pms2_related_(hpmsr6)_mrna,_complete_cds
u43586_1531-2101,kinase_suppressor_of_ras-1_(ksr1)_mrna,_partial_cds_
u43747_993-1425,frataxin_(frda)_mrna,_complete_cds_
u50839_1969-2413:not_in_gb_record,g16_protein_(g16)_mrna,_partial_cds.

20 u52513_1318-1642,rig-g_mrna,_complete_cds
u65533_3076-3620,regulator_of_nonsense_transcript_stability_(rent1)_mrna,_complete_cds_
u66828_2341-2500,carnitine_palmitoyltransferase_i_(cpti)_mrna,_complete_cds
u70867_3444-3936,prostaglandin_transporter_hpgt_mrna,_complete_cds_
u75362_2155-2557,isopeptidase_t-3_(isot-3)_mrna,_complete_cds

25 u92971_1235-1805,protease-activated_receptor(par3)_mrna,_complete_cds.
u93049_1841-2375,slp-76_associated_protein_mrna,_complete_cds
x01038mrna_285-824,fetal_gene_for_apolipoprotein_ai_precursor_
x14445exon#3_240-702,int-2_proto-oncogene
all_x14789_1204-1793,alpha-a_crystallin_gene_exon_1,2_and_pseudoexon_

30 x15357cds_2853-3135:in_reversesequence,_3262-3454,mrna_for_natriuretic_peptide_receptor_(anp-
a_recep
x71874cds#1_268-739:in_reversesequence,_4531-4534,_proteasome-like_subunit_mecl-
1_gene_extracted_fro
x84746cds_544-1012,histo-blood_group_ab0_gene,_exon_1

35 all_x85137_3131-3726,mrna_for_kinesin-related_protein
x98833mrna_3475-3937,mrna_for_zinc_finger_protein,_hsal1
all_y10260_1483-2048,eyal1_gene_
z30643cds_1860-1921,mrna_for_chloride_channel_(putative)_2139bp
z46967cds_1216-1714,mrna_for_calicin_(partial)_

Metagene 384

x92689cds_1457-1853,mrna_for_udp-galnac:polypeptide_n-
5 acetylgalactosaminyl_transferase/gb=x92689_nt

Metagene 392

d49728_2002-2330,nak1_mrna_for_dna_binding_protein,_complete_cds_
10 l10717_6303-6332,t_cell-specific_tyrosine_kinase_mrna,_complete_cds_
 l25119_1561-2119,mu_opiate_receptor_(mor1)_mrna,_complete_cds
 m32304_423-983,metalloproteinase_inhibitor_mrna,_complete_cds
 m84526_470-890,adipsin/complement_factor_d_mrna,_complete_cds
 u44103_339-559,small_gtp_binding_protein_rab9_mrna,_complete_cds.
15 u60319_2133-2643,hereditary_haemochromatosis_protein_hla-h_mrna,_complete_cds
 u63825_269-737,hepatitis_delta_antigen_interacting_protein_a_(dipa)_mrna,_complete_cds_
 u77735_1516-2026,pim-2_protooncogene_homolog_pim-2h_mrna,_complete_cds_
 u90544_1665-2145,sodium_phosphate_transporter_(npt3)_mrna,_complete_cds
 all_x76092_1925-2460,hrfx3_mrna
20 z22780cds_1528-1774:in_reversesequence,_1780-1870,cylicin_mrna

Metagene 73

ab000466_2465-2963,_clone_res4-24c,_exon_1,_2,_3
25 aj001487_25-265,mrna_for_transformation-sensitive_protein,_3'_utr/gb=aj001487_ntype=rna
 hg4755-ht5203_s_at_hg4755-ht5203_spinal_muscular_atrophy
 j03260mrna_2076-2576,transducin_alpha-subunit_(gnaz)_mrna,_complete_cds
 all_m20530_85-212,pancreatic_secretory_trypsin_inhibitor_(pti)_gene_
 m59911_4048-4612,integrin_alpha-3_chain_mrna,_complete_cds
30 m62400_1400-1928,gamma-aminobutyric_acid_receptor_type_a_rho-1_subunit_(gaba-a_rho-
 1)_mrna,_complete
 m74826_1928-2396,glutamate_decarboxylase_(gad-2)_mrna,_complete_cds
 all_u01317_19502-63478,_epsilon-
 globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsilon
35 u13220_1586-2066,forkhead_protein_freac-2_mrna,_partial_cds
 u54999_1795-2287,lgn_protein_mrna,_complete_cds
 all_x00734_8016-8239,beta-tubulin_gene_(5-beta)_with_ten_alu_family_members
 x65293cds_1670-2180,mrna_for_protein_kinase_c-epsilon
 all_x71348_2835-3436,vhnfl-c_mrna

all_x76057_1206-1765,pmil_mrna_for_phosphomannose_isomerase
 all_x98311_1901-2274,mrna_for_carcinoembryonic_antigen,_cgm2_
 z49205mrna_2454-2976,mrna_for_purinergic_receptor

5 Metagene 428

hg3344-ht3521_at_hg3344-ht3521_ubiquitin-conjugating_enzyme_ubch5
 all_m35999_3904-4463,platelet_glycoprotein_iiia_(gpIIIA)_mrna,_complete_cds
 all_u19906_5284-5711,arginine_vasopressin_receptor(avpr1)_gene,_complete_cds
10 u54617_1233-1737,pyruvate_dehydrogenase_kinase_isoformmrna,_complete_cds
 x94703cds_244-628:in_reversesequence,_640-748,rab28_mrna

Metagene 224

15 hg3859-ht4129_at_hg3859-ht4129_mage-4a_antigen_
 u61741_25-137,clone(hl-
 18)_dynein_heavy_chain_(dnahc14)_mrna,_partial_cds/gb=u61741_/ntype=rna
 u67784_1106-1640,orphan_g_protein-coupled_receptor_(rdc1)_mrna,_partial_cds

20 Metagene 437

all_m73548_9853-10274,polyposis_locus_(dp2.5_gene)_mrna,_complete_cds
 u30245exon_3-
 56,myelomonocytic_specific_protein_(mnida)_gene,_5'_flanking_sequence_and_complete_exon/
25 u36448_1252-1792,ca2+-dependent_activator_protein_for_secretion_mrna,_complete_cds_
 u41737_103-
 523,pancreatic_beta_cell_growth_factor_(ingap)_mrna,_complete_cds/gb=u41737_/ntype=rna
 u48697_1787-2276,mariner-like_element-containing_mrna,_clone_pchmt2
 x89986cds_271-387:in_reversesequence,_794-1043,mrna_for_nbk_apoptotic_inducer_protein_

30

Metagene 216

101087_2189-2693,protein_kinase_c-theta_(prkct)_mrna,_complete_cds_
 m16652mrna_324-
35 858,pancreatic_elastase_iiia_mrna,_complete_cds,pancreatic_elastase_iiia_mrna,_complete
 m27691_1901-2417,transactivator_protein_(creb)_mrna,_complete_cds
 m94893_989-1499,testis-specific_protein_(tspy)_mrna,_3'_end,_clone_pja923
 u30610_239-749,cd94_protein_mrna,_complete_cds_
 all_x17094_3675-4180,fur_mrna_for_furin

x55019cds_1128-1521:in_reversesequence,_1538-
1701,mrna_for_acetylcholine_receptor_delta_subunit.

Metagene 449

5

d79988_6383-6899,mrna_for_kiaa0166_gene,_complete_cds
d80001_4465-4939,mrna_for_kiaa0179_gene,_partial_cds_
d87450_5572-6034,mrna_for_kiaa0261_gene,_partial_cds_
hg2573-ht2669_at_hg2573-ht2669_zinc_finger_protein_kup_
10 m22638exon#4_154-682,lyl-1_protein_gene,_complete_cds
m62402_453-927,insulin-like_growth_factor_binding_protein(igfbp6)_mrna,_complete_cds
m85164_1354-1852,srf_accessory_protein_1b_(sap-1)_mrna,_complete_cds
s79873_3394-3969,_h-lamp-2=lysosome-associated_membrane_protein-
2_{alternatively_spliced}_[human,_li
15 u15174_224-746,nip3_(nip3)_mrna,_complete_cds
u24186cds_465-747:in_reversesequence,_1223-
1391,replication_protein_a_complex_subunit_homolog_rpa4_g
u34976_1059-1575,gamma-sarcoglycan_mrna,_complete_cds
u47677mrna_2495-2636,transcription_factor_e2f1_(e2f1)_gene,_promoter_and_
20 u59914_802-1240,chromosomemad_homolog_smad6_mrna,_complete_cds_
u80628_2216-2588,thymidine_kinaseisoform_b_(tk2)_mrna,_alternatively_spliced,_partial_cds_
all_x16323_5339-5814,mrna_for_hepatocyte_growth_factor_(hgf)_
x52009cds_813-1315:in_reversesequence,_1629,alpha-
1_strychnine_binding_subunit_of_inhibitory_glycine

25

Metagene 491

hg3510-ht3704_at_hg3510-ht3704_v-erba_related_ear-3_protein
hg880-ht880_s_at_hg880-ht880_mucin_6,_gastric
30 u37519_2304-2784,aldehyde_dehydrogenase_(aldh8)_mrna,_complete_cds_
all_x98263_520-1019,mrna_for_m-phase_phosphoprotein,_mpp6

Metagene 429

35 d13628_2506-2998,mrna_for_kiaa0003_gene,_complete_cds
hg2171-ht2241_r_at_hg2171-ht2241_12-lipoxygenase_
147726_2090-2552,phenylalanine_hydroxylase_(pah)_mutant_q20stop_mrna
all_m11591_5495-6174,in_m11591cds_567-598,mhc_ii_hla-sx-alpha_gene
u55764_784-1072,estrogen_sulfotransferase_mrna,_partial_cds

all_x51362_2101-2583,mrna_for_dopamine_d2_receptor_
x60708mrna_2812-3364,pchdp7_mrna_for_liver_dipeptidyl_peptidase_iv_

Metagene 210

5

j04111exon#1_2735-3251,c-jun_proto_oncogene_(jun),_complete_cds,_clone_hcj-1_
m19154mrna_2143-2503,transforming_growth_factor-beta-2_mrna,_complete_cds
m55210mrna#1_7322-7844,laminin_b2_chain_(lamb2)_gene_
m93426_7455-7845,protein_tyrosine_phosphatase_zeta-polypeptide_(ptprz)_mrna,_complete_cds
10 u04636mrna_3882-4386,cyclooxygenase-2_(hcox-2)_gene,_complete_cds_
u32114_756-1278,caveolin-2_mrna,_complete_cds
u60805_3576-4146,ontostatin-m_specific_receptor_beta_subunit_(osmrb)_mrna,_complete_cds

Metagene 208

15

d14686mrna_1554-2046,gene_for_glycine_cleavage_system_t-protein
d14695_1259-1817,mrna_for_kiaa0025_gene,_complete_cds
d23673_1204-
1666,_clone_hh109_(screened_by_the_monoclonal_antibody_of_insulin_receptor_substrate-1_(
20 d86965_6166-6490,mrna_for_kiaa0210_gene,_complete_cds
d89667_440-1004,mrna_for_c-myc_binding_protein,_complete_cds_
hg2379-ht3996_s_at_hg2379-ht3996_serine_hydroxymethyltransferase,_cytosolic,_altslice_2_
hg270-ht270_at_hg270-ht270_lymphocyte_chemoattractant_factor_
hg2868-ht3012_s_at_hg2868-ht3012_xe7,_pseudoautosomal_gene,_altslice_2
25 hg371-ht1063_s_at_hg371-ht1063_mucin_1,_epithelial,_altslice_6
hg3936-ht4206_at_hg3936-ht4206_interleukinreceptor
j00287exon#1_8-248:not_in_gb_record,pepsinogen_gene_
102867_2179-2689,62_kda_paraneoplastic_antigen_mrna,_3'_end_
113744_2775-3345,af-9_mrna,_complete_cds_
30 l14927exon#7_1-159,in_reversesequence,_5382-
5676,tear_prealbumin_(tp)_gene,_complete_cds_and_promote
l38935mrna_564-1026,gt212_mrna
m14218mrna_1044-1440,argininosuccinate_lyase_mrna,_complete_cds
m38449_40-599,transforming_growth_factor-beta_mrna,_complete_cds,_clone_ptgf-beta-trp114_
35 m57763_731-1151,adp-ribosylation_factor_(harf6)_mrna,_complete_cds_
m60278_1771-2221,heparin-binding_egf-like_growth_factor_mrna,_complete_cds_
m79462_3853-4333,pml-1_mrna,_complete_cds
m91196_938-1513,dna-binding_protein_mrna,_complete_cds_
m96326mrna_370-886,azurocidin_gene,_complete_cds

m96739_1964-2510,nscl-1_mrna_sequence
 s72043mrna_5-68,_gif=growth_inhibitory_factor_[human,_brain,_genomic,_2015_nt]_
 s82362_1119-1690,_hrar_beta_2=retinoic-acid-
 receptor_beta/suspected_tumor_suppressor_{5' region, tr

5 u03494_2213-2393,transcription_factor_lsf_mrna,_complete_cds_
 u05875_1655-2105,clone_psk1_interferon_gamma_receptor_accessory_factor-1_(af-
 1)_mrna,_complete_cds_
 u40714_692-1142,tyrosyl-trna_synthetase_mrna,_complete_cds/gb=u40714_/ntype=rna
 u41068cds_2-268:in_reversesequence,_944-

10 1155,retinoid_x_receptor_beta_(rxrbeta)_gene,_partial_3'_tra
 u47101_428-758,nifu-like_protein_(hnifu)_mrna,_partial_cds_
 u52112mrna#1_3929-
 4463,xq28_genomic_dna_in_the_region_of_the_11cam_locus_containing_the_genes_for_ne
 u54644_1437-1806,tub_homolog_mrna,_complete_cds

15 15 u58087_2096-2462,hs-cul-1_mrna,_complete_cds_
 u62531_3465-4029,ae2_anion_exchanger_(slc4a2)_mrna,_complete_cds_
 u65785_4028-4442,150_kda_oxygen-regulated_protein_orp150_mrna,_complete_cds
 u72515_1279-1811,c3f_mrna,_complete_cds
 u79255_760-1180,x11_protein_mrna,_partial_cds

20 20 all_x13451_84-268,mrna_for_lymphocyte_lineage-restricted_mb-1_membrane_glycoprotein_c-
 term(m-mb-1_ho
 x13973cds_996-1356:in_reversesequence,_1770-
 1896,mrna_for_ribonuclease/angiogenin_inhibitor_(rai)_
 all_x16135_1552-2003,mrna_for_novel_heterogeneous_nuclear_rnp_protein_1_protein_

25 25 x66362cds_743-1097:in_reversesequence,_1121-1217,mrna_pctaire-
 3_for_serine/threonine_protein_kinase_
 all_x80818_3601-3860,mrna_for_metabotropic_glutamate_receptor_type_4_
 x85106_2196-2712,mrna_for_ribosomal_s6_kinase

30 30 Metagene 160

d14811_644-1124,mrna_for_kiaa0110_gene,_complete_cds_
 d14889_760-1240,mrna_for_small_gtp-binding_protein,_s10,_complete_cds
 d21878_816-1386,mrna_for_bst-1,_complete_cds_

35 35 hg3288-ht3465_at_hg3288-ht3465_xanthine_dehydrogenase
 j04102_1830-2184,erythroblastosis_virus_oncogene_homolog(ets-2)_mrna,_complete_cds
 l25798_1061-1589,3-hydroxy-3-methylglutaryl_coenzyme_a_synthase_mrna,_complete_cds
 i41349mrna_3238-3646,phospholipase_c_beta(plcb4)_mrna,_complete_cds
 m17219_758-1286,brain_guanine_nucleotide-binding_protein_alpha-i_subunit_mrna,_5'_end

u55054_3199-3697,k-cl_cotransporter_(hkcc1)_mrna,_complete_cds_
 u57094_502-1018,small_gtp-binding_protein_mrna,_complete_cds_
 u93091_4410-4806,toll_protein_homolog_mrna,_complete_cds_and_line-
 1_reverse_transcriptase_homolog,_p

5

Metagene 156

hg2887-ht3031_r_at_hg2887-ht3031_sry-related_hmg-boxprotein
 hg4099-ht4369_s_at_hg4099-ht4369_adrenergic_receptor_alpha_1b_
 10 104947_3659-
 4199,(clones_bt3.081.8,_bt3.129.5_and_bt4.169)_receptor_tyrosine_kinase_(kdr)_mrna,_3'_e
 m74088_8374-8717,apc_gene_mrna,_complete_cds_
 m96738cds_719-1221,somatostatin_receptor_subtype(sstr3)_gene,_complete_cds
 m99435_2069-2325,transducin-like_enhancer_protein_(tle1)_mrna,_complete_cds
 15 s72487_1134-1582,_orf1_5'_to_pd-ecgf/tp...orf2_5'_to_pd-
 ecgf/tp_[human,_epidermoid_carcinoma_cell_li
 u28043_1989-2499,plasma_membrane_na+/h+_exchanger_isoform(nhe3)_mrna,_complete_cds
 u28049_1684-2221,txb2_(txb2)_mrna,_complete_cds
 u51003_2591-3169,dlx-2_(dlx2)_mrna,_complete_cds_
 20 u62739_986-1430,branched-chain_amino_acid_aminotransferase_(eca40)_mrna,_complete_cds
 u72509mrna_2-255,alternatively_spliced_b8_(b7)_mrna,_partial_sequence/gb=u72509/_ntype=rna_
 u79300_930-1404,clone_23629_mrna_sequence
 all_x69654_4-422,mrna_for_ribosomal_protein_s26
 x79439cds_16-277,notch dna_sequence/gb=x79439/_ntype=dna/_annot=cds
 25 x82850cds_722-1090:in_reversesequence,_1108-1238,mrna_for_thyroid_transcript_factor_1_
 y00414cds_1266-1537:in_reversesequence,_1573-1785,mrna_for_tyrosine_hydroxylase_type_3
 all_y08265_1306-1834,mrna_for_dan26_protein,_partial_
 z49254cds_75-435:in_reversesequence,_549-651,l23-related_mrna_

30 Metagene 149

d00097exon#2_152-710,serum_amyloid_p_component_(sap)_gene_with_upstream_promoter_
 d14533_812-1322,mrna_for_xpac_protein
 d16815_1642-2086,mrna_for_ear-1r,_complete_cds_
 35 d87683_6419-6941,mrna_for_kiaa0243_gene,_partial_cds_
 hg2510-ht2606_at_hg2510-ht2606_ras-specific_guanine_nucleotide-releasing_factor
 j00314mrna#1_4079-4173,beta-tubulin_gene,_clone_m40
 j05200mrna_14740-15238,ryanodine_receptor_mrna,_complete_cds
 l11329_1162-1630,protein_tyrosine_phosphatase_(pac-1)_mrna,_complete_cds

112760exon#9_396-

721,phosphoenolpyruvate_carboxykinase_(pck1)_gene,_complete_cds_with_repeats
 all_l35263_3222-3721,csaids_binding_protein_(csbp1)_mrna,_complete_cds_
 m22976mma_21-303:in_reversesequence,_668-728,cytochrome_b5_mrna,_3'_end

5 m62397_3586-4126,colorectal_mutant_cancer_protein_mrna,_complete_cds_
 all_m83554_3167-3576,lymphocyte_activation_antigen_cd30_mrna,_complete_cds_
 m84424exon_1073-1217,cathepsin_e_(ctse)_gene_
 all_m93311_1950-2085,metallothionein-iii_gene,_complete_cds

s83549_19-571,_na+/h+_exchanger_isoform_nhe-

10 2_[human,_various_tissues,_mrna_partial,_595_nt]/gb=s835
 u02082_1643-2201,guanine_nucleotide_regulatory_protein_(tim1)_mrna,_complete_cds_
 u14528_2357-2807,sulfate_transporter_(ditd)_mrna,_complete_cds
 u18009_1900-2338,chromosome_17q21_mrna_clone_1f113_
 u19517_1692-2010,(apoargc)_long_mrna,_complete_cds_

15 u22680_6048-6558,x2_box_repressor_mrna,_complete_cds_
 u36601_2620-3166,heparan_n-deacetylase/n-sulfotransferase-2_mrna,_complete_cds_
 u49436_1303-1783,translation_initiation_factor(eif5)_mrna,_complete_cds_
 u53003_1093-1609,gt335_mrna,_complete_cds
 u73338_6615-7113,methionine_synthase_mrna,_complete_cds

20 u73682_2255-2651,meningioma-expressed_antigen(meal1)_mrna,_partial_cds_
 u78876_1789-2317,mek_kinasemrna,_complete_cds_
 u80811_1092-1536,lysophosphatidic_acid_receptor_homolog_mrna,_complete_cds_
 x02176cds_1397-1656:in_reversesequence,_1681-
 1859,mrna_fragment_for_complement_component_c9

25 x05997cds#1_726-1158:in_reversesequence,_1280-1316,mrna_for_gastric_lipase
 x51956mrna_1881-2397,eno2_gene_for_neuron_specific_(gamma)_enolase
 all_x60483_975-1171,h4/d_gene_for_h4_histone_
 x67325cds_31-337:in_reversesequence,_43-541,p27_mrna
 x67683cds_34-319:in_reversesequence,_13,mrna_for_keratin/gb=x67683/_ntype=rna

30 x68149exon#2_2249-2687,blr1_gene_for_burkitt_lymphoma_receptor_1_
 x85133mrna_2399-2897,rbq-1_mrna
 x85372cds_18-210:in_reversesequence,_19-115,mrna_for_sm_protein_f_
 all_x87342_2921-3456,mrna_for_giant_larvae_homolog_
 x90908cds_11-353,mrna_for_i-15p_(i-babp)_protein_

35 all_y00978_2012-2535,mrna_for_dihydrolipoamide_acetyltransferase_(pdc-e2)_(ec_2.3.1.12)
 y12393_346-819,mma_for_sr1-like_protein,_partial_
 z24459exon#1_13-
 199,_exon2a_frommtcp1_gene,_exons_2a_to(and_joined_mrna)/gb=z24459/_ntype=dna_/annot

Metagene 125

d14827_1564-1966,mrna_for_tax_helper_protein_1,_complete_cds_
all_d26561_2433-

5 3022,_orf_for_11_protein_gene_extracted_frompapillomavirus_5b_genome_integrated_into
l34060_2124-2502,cadherin-8_mrna,_complete_cds
m94167_1894-2326,heregulin-beta2_gene,_complete_cds
s83390_2318-2865,_t3_receptor-associating_cofactor-1_[human,_fetal_liver,_mrna,_2930_nt]
u03398_1069-1576,receptor_4-1bb_ligand_mrna,_complete_cds

10 u52152_2642-3020,inwardly_rectifying_potassium_channel_kir3.3_mrna,_complete_cds_
u64871cds_870-1212:in_reversesequence,_1665-1773,putative_g_protein-
coupled_receptor_(gpr19)_gene,_c
u95626mrna#2_1641-
2133,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_and_
15 x77094cds_634-994:in_reversesequence,_1136-1214,mrna_for_p40phox

Metagene 71

ab000220_4588-5134,mrna_for_semaphorin_e,_complete_cds_
20 109749_1019-1463,(clone_f4)_transmembrane_protein_mrna_sequence_
m87313_793-1335,myotonin_protein_kinase_(dm)_mrna_
u04520mrna_6221-6641,type_iv_collagen_a5_chain_(col4a5)_gene_
all_x87904_4159-4670,mrna_for_sep_protein
z78285_3-137,mrna_(clone_1a7)

25

Metagene 374

ab000896_49-391,mrna_for_cadherin_fib2,_partial_cds/gb=ab000896_/ntype=rna
ac002115mrna#1_932-

30 1448,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping_chromosomecosmids_r313
d29641_2800-3292,mrna_for_kiaa0052_gene,_partial_cds
d83699_623-1001,brain_3'_utr_of_mrna_for_neuronal_death_protein,_partial_sequence
d86960_5652-6168,mrna_for_kiaa0205_gene,_complete_cds
hg2152-ht2222_at_hg2152-ht2222_zinc_finger_protein_92

35 hg3707-ht3922_f_at_hg3707-ht3922_guanine_nucleotide-
binding_protein,_alpha_inhibiting_activity_polyp
113994_2830-3196,prec_gene,_complete_cds;_orf_x,_complete_cds_
122343_1136-1517,nuclear_phosphoprotein_mrna,_complete_cds_
141607mrna_1772-2330,beta-1,6-n-acetylglucosaminyltransferase_(ignt)_gene

all_m11437_1562-2440:in_m11437cds#1_1198-
 1226_kng_gene_(kininogen)_extracted_fromkininogen_gene,_kn
 m27533_883-1451,ig_rearranged_b7_protein_mrna_vc1-region,_complete_cds.
 m61764mrna_1015-1495,gamma-tubulin_mrna,_complete_cds

5 m65085_1792-2302,follicle_stimulating_hormone_receptor_mrna,_complete_cds
 m81778_2123-2689,serotonin_5-ht1c_receptor_mrna,_complete_cds
 s66541cds_375-687:in_reversesequence,_99-314,_b-
 50=neural_phosphoprotein_[human,_genomic,_1845_ntseg
 u03911_2485-3013,mutator_gene_(hmsh2)_mrna,_complete_cds_

10 u22816_3784-4288,lar-interacting_protein_1b_mrna,_complete_cds_
 u51095_1230-1656,homeobox_protein_cdx1_mrna,_complete_cds
 u59748_28-187,desert_hedgehog_(hdhh)_mrna,_partial_cds/gb=u59748_/ntype=rna
 u61538_199-751,calcium-binding_protein_chp_mrna,_complete_cds
 u74324_1797-2349,guanine_nucleotide_exchange_factor_mss4_mrna,_complete_cds

15 u81787_1686-2238,wnt10b_mrna,_complete_cds.
 u90437_43-259,rp1_homolog_mrna,_3'_utr_region/gb=u90437_/ntype=rna_
 all_x04391_1779-2320,mrna_for_lymphocyte_glycoprotein_t1/leu-1_
 x15673mrna_623-1121,ptr2_mrna_for_repetitive_sequence/gb=x15673_/ntype=rna_
 all_x15949_1543-2144,mrna_for_interferon_regulatory_factor-2_(irf-2)_

20 x56667mrna_915-1341,mrna_for_calretinin
 x78924cds_55-466:in_reversesequence,_622-631,hzfl1_mrna_for_zinc_finger_protein
 x97630_2420-2897,mrna_for_serine/threonine_protein_kinase_emk
 all_x99657_783-1318,mrna_for_protein_containing_sh3_domain,_sh3gl2_

25 Metagene 168

d00761_252-750,mrna_for_proteasome_subunit_hc5_
 d00762_237-777,mrna_for_proteasome_subunit_hc8_
 d13435_526-832,mrna_for_pig-f_(phosphatidyl-inositol-glycan_f),_complete_cds_

30 d13969_1638-2148,mrna_for_mel-18_protein,_complete_cds_
 d29677_5709-6231,mrna_for_kiaa0054_gene,_complete_cds
 d31762_6385-6775,mrna_for_kiaa0057_gene,_complete_cds
 d31766_2024-2552,mrna_for_kiaa0060_gene,_complete_cds
 d38449_2311-2791,mrna_for_g_protein-coupled_receptor,_complete_cds_

35 d38535_2583-2973,mrna_for_pk-120_
 d43950_1355-1739,mrna_for_kiaa0098_gene,_partial_cds_
 d50487_3756-4098,mrna_for_rna_helicase_(hrh1),_complete_cds
 d50863_1908-2370,mrna_for_tesk1,_complete_cds
 d50922_1972-2452,mrna_for_kiaa0132_gene,_complete_cds

d50923_5018-5528,mrna_for_kiaa0133_gene,_complete_cds
d78586_6497-6923,cad_mrna_for_multifunctional_protein_cad,_complete_cds
d79993_2741-3167,mrna_for_kiaa0171_gene,_complete_cds
d79997_1881-2415,mrna_for_kiaa0175_gene,_complete_cds
5 d80010_4778-5198,mrna_for_kiaa0188_gene,_partial_cds_
d83776_4596-5166,mrna_for_kiaa0191_gene,_partial_cds_
d83782_3411-3915,mrna_for_kiaa0199_gene,_partial_cds_
d84557_2412-2874,mrna_for_hsmcm6,_complete_cds_
d86968_4437-4899,mrna_for_kiaa0213_gene,_partial_cds_
10 d86971_4851-5325,mrna_for_kiaa0217_gene,_partial_cds_
d86976_3592-4060,mrna_for_kiaa0223_gene,_partial_cds_
hg1019-ht1019_at_hg1019-ht1019_serine_kinase_pska-h1
hg1879-ht1919_at_hg1879-ht1919_ras-like_protein_tc10_
hg2190-ht2260_at_hg2190-ht2260_crystallin_beta_b3_
15 hg2379-ht3997_s_at_hg2379-ht3997_serine_hydroxymethyltransferase,_cytosolic,_altslice_3_
hg2649-ht2745_s_at_hg2649-ht2745_serine/threonine_protein_kinase_cdk3
hg3033-ht3194_r_at_hg3033-ht3194_spliceosomal_protein_sap_62_
hg3327-ht3504_s_at_hg3327-ht3504_dna-binding_protein_hrfx2_
hg3945-ht4215_at_hg3945-ht4215_phospholipid_transfer_protein_
20 hg4094-ht4364_s_at_hg4094-ht4364_transcription_factor_lsf-id_
hg4433-ht4703_at_hg4433-ht4703_cyclin_d1_promoter
hg511-ht511_at_hg511-ht511_ras_inhibitor_inf_
all_j03764_14604-15049,_human,_plasminogen_activator_inhibitor-1_gene,_exonsto_9_
104953_2585-3065,x11_protein_(x11)_mrna,_3'_end
25 109260_781-1171,(chromosome_3p25)_membrane_protein_mrna
111284_1672-2122,_homosapiens_erk_activator_kinase_(mek1)_mrna
112711_1468-2000,transketolase_(tk)_mrna,_complete_cds
116991_679-1132,thymidylate_kinase_(cdc8)_mrna,_complete_cds_
125286_4549-5081,alpha-1_type_xv_collagen_mrna,_complete_cds
30 132976_2969-3533,protein_kinase_(mlk-3)_mrna,_complete_cds_
136529mrna_1491-2043,(clone_n5-4)_protein_p84_mrna,_complete_cds_
136983mrna_3012-3546,dynamin_(dnm)_mrna,_complete_cds_
137347_1301-1835,integral_membrane_protein_(nramp2)_mrna,_partial
all_m13241_5990-6537,n-myc_gene,_exonsand_3_
35 all_m15205_12942-
13411,thymidine_kinase_gene,_complete_cds,_with_clustered_alu_repeats_in_the_intron
m16707mrna_6-
357,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_clone_fo1
m20747_1519-2034,insulin-responsive_glucose_transporter_(glut4)_mrna,_complete_cds_

m21121_958-1129,t_cell-specific_protein_(rantes)_mrna,_complete_cds
m21154mrna_1234-1756,s-adenosylmethionine_decarboxylase_mrna,_complete_cds_
m23668exon_743-1271,adrenodoxin_gene
m24470mrna_911-1355,glucose-6-phosphate_dehydrogenase,_complete_cds
5 m25280_1753-2299,lymph_node_homing_receptor_mrna,_complete_cds_
m28249_4850-5306,very_late_antigen-2_(vla-2)/collagen_receptor_alpha-
2_subunit_mrna,_complete_cds
m29536_1025-1361,translational_initiation_factorbeta_subunit_(elf-2-beta)_mrna,_complete_cds
m34539_1051-1477,fk506-binding_protein_(fkbp)_mrna,_complete_cds_
10 m38591_120-600,cellular_ligand_of_annexin_ii_(p11)_mrna,_complete_cds_
m54915_2208-2236,h-pim-1_protein_(h-pim-1)_mrna,_complete_cds
m60091_1118-1248,galactose-1-phosphate_uridyl_transferase_mrna,_complete_cds_
m60450_1932-2404,voltage-gated_potassium_channel_(hk1)_mrna,_complete_cds
m60527mrna_1877-2369,deoxycytidine_kinase_mrna,_complete_cds_
15 m63180_2055-2505,threonyl-trna_synthetase_mrna,_complete_cds_
m69013_1053-1515,guanine_nucleotide-binding_regulatory_protein_(g-y-
alpha)_mrna,_complete_cds
m69039_625-1171,pre-mrna_splicing_factor_sf2p32,_complete_sequence_
m86852_1041-1557,peroxisome_assembly_factor-1_mrna,_complete_cds_
20 m87339_875-1361,replication_factor_37-kda_subunit_mrna,_complete_cds
m87434_2316-2862,71_kda_2'_5'_oligoadenylate_synthetase_(p69_2-
5a_synthetase)_mrna,_complete_cds_
s77356_3-
41,_transcript_ch21=oligomycin_sensitivity_conferral_protein_oscop_homolog_[human,_rf1,rf48_
25 s78187_2548-3064,_cdc25hu2=cdc25+_homolog_[human,_mrna,_3118_nt]
u04810_2050-2536,tastin_mrna,_complete_cds_
u05681exon#7_111-544,proto-oncogene_bcl3_gene
u10362_848-1352,gp36b_glycoprotein_mrna,_complete_cds
u14391_4095-4623,myosin-ic_mrna,_complete_cds
30 u15131_3802-4252,p126_(st5)_mrna,_complete_cds_
u20428_2450-2840,snc19_mrna_sequence_
u24704_790-1264,antisecretory_factor-1_mrna,_complete_cds
u29607_1974-2148,methionine_aminopeptidase_mrna,_complete_cds
u34683_1261-1735,glutathione_synthetase_mrna,_complete_cds_
35 u41668_520-976,deoxyguanosine_kinase_mrna,_complete_cds
u52828_1418-1882,cri-du-chat_region_mrna,_clone_niba2
u53347_2278-2812,neutral_amino_acid_transporter_b_mrna,_complete_cds_
u56402_2969-3471,chromatin_structural_protein_homolog_(supt5h)_mrna,_complete_cds
u58766_741-1299,fx_protein_mrna,_complete_cds

u59752_524-938,sec7p-like_protein_mrna,_partial_cds
 u59919_2047-2575,smg_gds-associated_protein_smap_mrna,_complete_cds
 u60325_3700-
 4252,dna_polymerase_gamma_mrna,_nuclear_gene_encoding_mitochondrial_protein,_complete_cd
5 u62293mrna_2576-3152,_limk1_gene_(lim-kinase1)_extracted_fromlim-
 kinase1_and_alternatively_spliced_1
 u69127_2758-3106,fuse_binding_protein(fbp3)_mrna,_partial_cds_
 u71374_617-1157,hspex13p_mrna,_complete_cds/gb=u71374_/ntype=rna_
 all_u73167_4971-
10 35099,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted_from
 u83463_1406-1862,scaffold_protein_pbp1_mrna,_complete_cds
 u86070_629-1205,phosphomannomutase_mrna,_complete_cds
 u87269_1976-2468,p120e4f_transcription_factor_mrna,_complete_cds.
 u91985_1014-1320,dna_fragmentation_factor-45_mrna,_complete_cds
15 u94319_2044-2404,autoantigen_dfs70_mrna,_partial_cds.
 all_x03794_570-1150,embryonic_mrna_3'_end_with_homoeo_box_(clone_hhoc10)_
 all_x05299_2010-2572,mrna_(~95%)_for_major_centromere_autoantigen_cenp-b_
 all_x06389_1582-2087,mrna_for_synaptophysin_(p38)
 all_x07695_1175-1722,mrna_for_cytokeratinc-terminal_region
20 all_x15331_813-1194,mrna_for_phosphoribosylpyrophosphate_synthetase_subunit_one
 x15722cds_931-1411:in_reversesequence,_1569-1575,mrna_for_glutathione_reductase_(ec_1.6.4.2)
 x15822cds_18-222:in_reversesequence,_13-379,cox_viiia-1_mrna_for_liver-
 specific_cytochrome_c_oxidase_
 x17620mrna_257-
25 677,mrna_for_nm23_protein,_involved_in_developmental_regulation_(homologto_drosophila
 x54637cds_3359-3539:in_reversesequence,_3857-4133,tyk2_mrna_for_non-
 receptor_protein_tyrosine_kinase
 all_x59727_3618-4201,63_kda_protein_kinase_related_to_rat_erk3_
 x63417cds_170-524:in_reversesequence,_560,irlb_mrna_
30 all_x63522_1800-1997,mrna_daudi6_for_retinoic_acid_x_receptor_b
 x63657mrna_1683-2169,fvt1_mrna_
 x63679cds_587-1073,mrna_for_tramp_protein
 all_x69115_718-998,znf37a_mrna_for_zinc_finger_protein_
 x71129cds_213-705,mrna_for_electron_transfer_flavoprotein_beta_subunit_
35 x74330cds_788-1154:in_reversesequence,_1281-1335,mrna_for_dna_primase_(subunit_p48)_
 x74801cds_1282-1552:in_reversesequence,_1636-1837,cctg_mrna_for_chaperonin
 x74874mrna_5857-
 6262,_rna_polymerase_ii_largest_subunit_gene_extracted_fromgene_for_rna_pol_ii_large
 x78992cds_1349-1373,erf-2_mrna_

all_x80910_3085-3566,ppp1cb_mrna_
 x81788_397-799,ds-1_mrna_
 x92720cds_1540-1888:in_reversesequence,_1978-
 2086,mrna_for_phosphoenolpyruvate_carboxykinase
5 x93510cds_548-956:in_reversesequence,_1021-1069,mrna_for_37_kda_lim_domain_protein
 x97544cds_291-453:in_reversesequence,_508-724,mrna_for_tim17_preprotein_translocase_
 x98248mrna_3140-3698,mrna_for_sortilin
 x98534exon#10_287-798,vasp_gene,_exonsto_13_
 x99947_2580-2922:in_reversesequence,_2994-3084,mrna_dynein-related_protein
10 y00636cds_586-688:in_reversesequence,_739-
 985,mrna_for_lymphocyte_function_associated_antigen-3_(lfa
 all_y11681_529-1040,mrna_for_mitochondrial_ribosomal_protein_s12/gb=y11681_/ntype=rna_
 z23064_1461-1755,mrna_gene_for_hnrnp_g_protein_
 all_z48042_2679-3232,mrna_encoding_gpi-anchored_protein_p137_
15 all_z70219_4-188,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507c0696)
 z84497cds_1915-2230:in_fullsequence,_18383-
 18624,dna_sequence_from_cosmid_o14_on_chromosomecontains_

Metagene 388

20
 d38128exon_604-1126,ip_gene_for_prostacyclin_receptor
 d43638_2961-3393,mrna_for_mtg8a_protein,_complete_cds
 hg2167-ht2237_at_hg2167-ht2237_protein_kinase_ht31,_camp-dependent_
 hg2715-ht2811_at_hg2715-ht2811_tyrosine_kinase_
25 hg3492-ht3686_at_hg3492-ht3686_uncoupling_protein_ucp
 l11373_4183-4609,protocadherin_43_mrna,_complete_cds_for_abbreviated_pc43
 l34409_624-990,(clone_b3b3e13)_chromosome_4p16.3_dna_fragment_
 l36645mrna_2716-3034,receptor_protein-tyrosine_kinase_(hek8)_mrna,_complete_cds_
 m16801mrna_5250-5724,mineralocorticoid_receptor_mrna_(hmr),_complete_cds_
30 m60556mrna#1_503-839,_tgfb3_gene_(transforming_growth_factor-beta_3)_extracted_fromtransforming_grow
 m74096_1694-2096,long_chain_acyl-coa_dehydrogenase_(acadl)_mrna,_complete_cds
 m97676_1406-1646,(region_7)_homeobox_protein_(hox7)_mrna,_complete_cds
 s73840_408-
35 784,_type_iix_myosin_heavy_chain_{3'_region}_[_human,_skeletal_muscle,_mrna_partial,_827_n
 s81661_588-1164,_keratinocyte_growth_factor_[human,_mrna,_1200_nt]
 u02683_2758-3318,alpha_palindromic_binding_protein_mrna,_complete_cds
 u08096exon_31-481,peripheral_myelin_protein-22_(pmp22)_gene,_non-coding_exon_1b/gb=u08096_/ntype=dna

u37122_1877-2387,adducin_gamma_subunit_mrna,_complete_cds
 u44754_809-1253,pse-binding_factor_ptf_gamma_subunit_mrna,_complete_cds
 u69546_1903-2299,rna_binding_protein_etr-3_mrna,_complete_cds
 u79251_1285-1747,clone_23878_mrna_sequence_
5 all_x04325_1113-1558,liver_mrna_for_gap_junction_protein_
 all_x59350_2679-3220,mrna_for_b_cell_membrane_protein_cd22_
 x67697cds_1-145:in_reversesequence,_63-603,he2_mrna_

Metagene 378

10

d87011cds_1308-1590:in_fullsequence,_24060-
 24222,(lamuda)_dna_for_immunoglobulin_light_chain_
 j04156mrna_1030-1510,interleukin(il-7)_mrna,_complete_cds_
 s95936_1806-2268,_transferrin_[human,_liver,_mrna,_2347_nt]_
15 u24153_1796-1994,p21-activated_protein_kinase_(pak2)_gene,_complete_cds

Metagene 359

20

d86975_5570-5978,mrna_for_kiaa0222_gene,_complete_cds
 105514cds_20-116:in_reversesequence,_1789-1815:not_in_gb_record,histatin(his2)_gene_
 all_x83857_1431-1809,mrna_for_prostaglandin_e_receptor_(ep3a1)_

Metagene 261

25

hg274-ht274_s_at_hg274-ht274_gamma-glutamyltransferase
 u49379_2051-2537,diacylglycerol_kinase_epsilon_dgk_mrna,_complete_cds
 u81607_6007-6535,gravin_mrna,_complete_cds_
 all_x81479_2655-3118,mrna_for_emr1_hormone_receptor
 x86816mrna_4-193,estrogen_receptor_cdna,_5'_splice_variant/gb=x86816/_ntype=rna

30

Metagene 234

u50822mrna_909-1375,neurogenic_helix-loop-helix_protein_neurod_(neurod)_gene,_complete_cds
 u68030_2365-2665,g_protein-coupled_receptor_(strl22)_mrna,_complete_cds
35 all_u77827_1053-1630,orphan_g_protein-coupled_receptor_(cepr)_gene,_complete_cds.
 all_x77366_4160-4689,hbz17_mrna

Metagene 227

aj001047cds_485-791:in_reversesequence,_959-1013,mrna_for_matrilin-3/gb=aj001047_/ntype=rna
 d25216_4968-5256,mrna_for_kiaa0014_gene,_complete_cds
 d29012_230-752,mrna_for_proteasome_subunit_y,_complete_cds_
 d29954_4458-4920,mrna_for_kiaa0056_gene,_partial_cds_

5 d45906_3097-3613,mrna_for_link-2,_complete_cds_
 d50810_3494-3992,mrna_for_placental_leucine_aminopeptidase,_complete_cds_
 d50913_1494-2052,mrna_for_kiaa0123_gene,_partial_cds_
 d63160exon_6-306:in_reversesequence,_9:not_in_gb_record,dna_for_lectin_p35_
 d83703_2605-3169,mrna_for_peroxisome_assembly_factor-2,_complete_cds_

10 d90042_675-1215,liver_arylamine_n-acetyltransferase_(ec_2.3.1.5)_gene
 hg2036-ht2090_at_hg2036-ht2090_stimulatory_gdp/gtp_exchange_protein_for_c-ki-
 ras_p21_and_smg_p21_
 hg2566-ht4867_at_hg2566-ht4867_microtubule-associated_protein_tau,_altslice_5,_exon_4a'
 hg2706-ht2802_at_hg2706-ht2802_serine/threonine_kinase_

15 hg3976-ht4246_at_hg3976-ht4246_pou-domain_dna_binding_factor_pit1,_pituitary-specific
 hg870-ht870_at_hg870-ht870_golgin_165_kda_polypeptide_
 hg909-ht909_at_hg909-ht909_mg81
 j02876mrna_616-1180,placental_folate_binding_protein_mrna,_complete_cds
 105147_266-812,dual_specificity_phosphatase_tyrosine/serine_mrna,_complete_cds_

20 l10405_1364-
 1910,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds/gb=l10405_/ntype=rn
 114754_3369-3813,dna-binding_protein_(smbp2)_mrna,_complete_cds
 119058_2599-3163,glutamate_receptor_(glur5)_mrna,_complete_cds_
 126494_1598-2084,(oct-6)_mrna,_complete_cds_

25 l29433exon_53-587,factor_x_(blood_coagulation_factor)_gene_
 136861exon#4_247-757,guanylate_cyclase_activating_protein_(gcap)_gene_exons_1-
 4,_complete_cds_
 all_l36922_938-1125,met-ase_gene,_exon_1
 140377mrna_766-1276,cytoplasmic_antiproteinase(cap2)_mrna,_complete_cds

30 l47738_2286-2856,inducible_protein_mrna,_complete_cds_
 all_m16652_714-
 760,pancreatic_elastase_ii_a_mrna,_complete_cds,pancreatic_elastase_ii_a_mrna,_complete
 m31651cds_900-1146:in_reversesequence,_5912-6098,human_sex_hormone-
 binding_globulin_(shbg)_gene,_com

35 all_m34041_1414-2015,alpha-2-adrenergic_receptor_(alpha-2_c2)_gene,_complete_cds_
 m35878exon#4_1993-2443,insulin-like_growth_factor-binding_protein-
 3_gene,_complete_cds,_clone_hl1006
 all_m58378_75-406:in_m58378cds#1_1893-
 1930:in_m58378cds#2_2002,_syn1_gene_(synapsin_i)_extracted_fro

m64595mrna_216-648,small_g_protein_(gx)_mrna,_3'_end_
m76180_1461-1887,aromatic_amino_acid_decarboxylase_(ddc)_mrna,_complete_cds
m86757_2-372,psoriasis_mrna,_complete_cds
m91438cds_55-181:in_reversesequence,_300-540,kazal-type_serine_proteinase_(husi-
5 ii)_gene,_complete_c
m93718_3536-4034,nitric_oxide_synthase_mrna,_complete_cds
m94077exon#2_657-1125,loricrin_gene_exonsand_2,_complete_cds
m94547mrna_55-565,_hummlc2at;_homo_sapiens;:_593_base-pairs
m95712_2005-2407,b-raf_mrna,_complete_cds
10 m98045_1593-2097,folylpolyglutamate_synthetase_mrna,_complete_cds_
all_s57887_739-
980,(t1)=elastin_translocation_allele_{exon_28,_translocation}{[human,_genomic_mutan
s67070_55-
421,heat_shock_protein_hsp72_homolog_[human,_thyroid_associated_ophthalmopathy_patient,_m
15 s82198_323-827,_caldecrin=serum_calcium-
decreasing_factor_[human,_pancreas,_mrna_partial,_894_nt]
u06088exon_220-730,n-acetylgalactosamine_6-sulphatase_(galns)_gene
u08191_4687-5220,r_kappa_b_mrna,_complete_cds
u09850_3337-3769,zinc_finger_protein_(znf143)_mrna,_complete_cds_
20 u13045_2126-2690,nuclear_respiratory_factor-2_subunit_betamrna,_complete_cds
all_u15177_2291-2724,cosmid_cri-jc2015_at_d10s289_in_10sp13
u22526_2677-3157,2,3-oxidosqualene-lanosterol_cyclase_mrna,_complete_cds_
u35234_6175-6290,protein_tyrosine_phosphatase_sigma_mrna,_complete_cds_
u41763_4933-5485,muscle_specific_clathrin_heavy_chain_(cltd)_mrna,_complete_cds
25 u42412_977-1535,S'_amp-activated_protein_kinase,_gamma-1_subunit_mrna,_complete_cds_
u48408_752-1322,kidney_water_channel_(hkid)_mrna,_complete_cds_
u49260_1284-1761,mevalonate_pyrophosphate_decarboxylase_(mpd)_mrna,_complete_cds_
u49395_1361-1907,ionotropic_atp_receptor_p2x5a_mrna,_complete_cds
u52112mrna#5_896-
30 1340,xq28_genomic_dna_in_the_region_of_the_l1cam_locusContaining_the_genes_for_neu
u55258cds_3452-3872:in_reversesequence,_4031-4091,hbravo/nr-cam_precursor_(hbravo/nr-
cam)_gene,_comp
all_u57341_2-
129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341/_ntype=rna,neurofilamen
35 u60666_1923-2415,testis_specific_leucine_rich_repeat_protein_(tslrp),_complete_cds_
u65402cds_651-915:in_reversesequence,_1437-1647,seven_transmembrane_g-
coupled_receptor_(gpr31)_gene,
u68485_1356-1788:not_in_gb_record,box-dependent_myc-interacting_protein-
1_(bin1)_mrna,_complete_cds_

u70064_6458-7030,lysosomal_trafficking_regulator_(lyst)_mrna,_partial_cds
 u72209_432-990,yy1-associated_factor(yaf2)_mrna,_complete_cds_
 u87964_1515-2094,putative_g-protein_(gp-1)_mrna,_complete_cds
 x00090cds_6-356,histone_h3_gene
5 all_x00695_6073-6372,interleukin-2_(il-2)_gene_and_5'_flanking_region_
 x01715cds_1338-
 1537:not_in_gb_record,gene_fragment_for_the_acetylcholine_receptor_gamma_subunit_prec
 x05360cds_353-785,cdc2_gene_involved_in_cell_cycle_control_
 all_x13810_1940-1986,otf-2_mrna_for_lymphoid-specific_transcription_factor_
10 x51952mrna_355-
 517,_ucp_fromucp_gene_for_uncoupling_protein_exonsand/gb=x51952/_ntype=dna/_annot=exo
 all_x63717_1962-2473,mrna_for_apo-1_cell_surface_antigen_
 x66839cds_909-1335:in_reversesequence,_1407-1491,matu_mm_mrna_for_p54/58n_protein_
 x69950exon#1_1485-2039,dna_sequence_for_wilms'_tumor_gene
15 all_x70297_1563-2020,mrna_for_neuronal_nicotinic_acetylcholine_receptor_alpha-7_subunit
 x77777_2210-2771,intestinal_vip_receptor_related_protein_mrna
 all_x96969_1470-1759,mrna_for_urea_transporter_
 x99656cds_798-1068:in_reversesequence,_1251-
 1329,mrna_for_protein_containing_sh3_domain,_sh3gl1_
20 reverse_y10871_4016-4220,twist_gene
 z25884cds_2453-2897:in_reversesequence,_3062-3068,mrna_for_clc-
 1_muscle_chloride_channel_protein
 z48475cds_1531-1795:in_reversesequence,_1918-2128,gckr_mrna_for_glucokinase_regulator_
 all_z69720_14484-
25 15067,dna_sequence_from_cosmid_ra36_from_a_contig_from_the_tip_of_the_short_arm_of
 all_z70220_31-266,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507o0882).
 reverse_z95624_34190-
 34542,dna_sequence_from_cosmid_u237h1_contains_ras_like_gtpase_and_est.

30 Metagene 217

 d17793_633-1161,mrna_for_kiaa0119_gene,_complete_cds_
 hg64-ht64_at_hg64-ht64_nf-kappa_b-binding_protein_kbp-1
 k03474exon#5_562-829:in_reversesequence,_2817-
35 2919,mullerian_inhibiting_substance_gene,_complete_cds
 l00022cds_1249-1679:in_reversesequence,_1750-1816,ig_active_epsilon1_5'_ut_v-d-
 j_region_subgroup_vh
 m31774_1858-2392,thyrotropin_receptor_(tsh)_mrna,_complete_cds_
 u58033_24-366,myotubularin_related_protein(mtmr2)_gene,_partial_cds/gb=u58033/_ntype=rna

x06290cds_13307-13442:in_reversesequence,_13709-13913,mrna_for_apolipoprotein(a)_
 x87843cds_690-894:in_reversesequence,_1045-1201,mrna_for_cyclin_h_assembly_factor_
 x99350mrna_1863-2424,_hfh4_cds_gene_extracted_fromhfh4_gene,_exonand_joined_cds

5 Metagene 66

d49824_945-1110,hla-b_null_allele_mrna,hla-b_null_allele_mrna_
 hg862-ht862_s_at_hg862-ht862_transition_protein_
 j04040mrna_563-1016,glucagon_mrna,_complete_cds
10 m15881_1752-2310,uromodulin_(tamm-horsfall_glycoprotein)_mrna,_complete_cds
 u77970_2339-2855,neuronal_pas2_(npas2)_mrna,_complete_cds
 x67318cds_851-1229:in_reversesequence,_1260,mrna_for_procarboxypeptidase_a1_

Metagene 60

15 u31382_69-621,g_protein_gamma-4_subunit_mrna,_complete_cds_
 x07820cds_1252-1378:in_reversesequence,_1430-1694,mrna_for_metalloproteinase_stromelysin-2
 x14329cds_1050-1350:in_reversesequence,_1569-
 1641,mrna_for_carboxypeptidase_n_small_subunit_(ec_3.4).
20 z47043cds_540-
 1080,partial_cdna_sequence,_clone_x529,_unknown_open_reading_frame;/gb=z47043_/ntype=d

Metagene 48

25 d26561cds#2_153-435:in_reversesequence,_3711-
 3717,_orf_for_11_protein_gene_extracted_frompapillomavi
 hg3703-ht3915_s_at_hg3703-ht3915_udp-
 glucuronosyltransferasefamily,_polypeptide_1,_altslice_1
 all_l37868_3521-4088,pou-domain_transcription_factor_(n-oct-3),_complete_cds
30 x74819cds_509-809:in_reversesequence,_913-1015,mrna_for_cardiac_troponin_t

Metagene 21

af012270_815-1325,peropsin_(rrh)_mrna,_complete_cds;/gb=af012270_/ntype=rna
35 l40411mrna_43-511,thyroid_receptor_interactor_(trip8)_mrna,_3'_end_of_cds_
 all_x64877_494-529,mrna_for_serum_protein,mrna_for_serum_protein

Metagene 17

d50931_2527-2971,mrna_for_kiaa0141_gene,_complete_cds
m97016_1231-1803,osteogenic_protein-2_(op-2)_mrna,_complete_cds.
s58544_1884-2382,_75_kda_infertility-
related_sperm_protein_[human,_testis,_mrna_partial,_2427_nt]_

5 s81737_1159-1681,_alphasyntrphin_[human,_mrna_partial,_1771_nt]_
u06233_2545-3055,pou_domain_protein_(brn-3b)_mrna,_complete_cds
u07681_2075-2585,nad(h)-
specific_isocitrate_dehydrogenase_alpha_subunit_precursor_mrna,_complete_cds
u68385_1259-1643,meis1-related_protein(mrg2),_mrna,_partial_cds.

10 u69108_2155-2632,tnf_receptor_associated_factormrna,_partial_cds_
all_x79066_390-973,_hsapiens_erf-1_mrna_5'_end
x91653exon_5-125,dna_for_exon_encoding_for_n-
acetylglucosaminyltransferase_v_(340_bp)/gb=x91653_/nty
y00083cds_902-1201:in_reversesequence,_1416-1641,mrna_for_glioblastoma-derived_t-
15 cell_suppressor_fac

Metagene 478

k02402exon#8_1383-1875,coagulation_factor_ix_gene,_complete_cds
20 141162_1879-2419,collagen_alphahtype_ix_(col9a3)_mrna,_complete_cds_
all_m21388_2-95,unproductively_rearranged_ig_mu-chain_mrna_v-region_(vd),_5'_end,_clone_mu-
3ala.,unp
all_m29610_446-476,glycophorin_e_mrna,_complete_cds,glycophorin_e_mrna,_complete_cds
u79286_934-1294,arginine_methyltransferase_mrna,_complete_cds

25

Metagene 313

ac002045mrna#1_643-838,_a-589h1.1_fromchromosomebac_clone_cit987-ska-
589h1_~complete_genomic_sequenc
30 aj000099_1243-1750,mrna_for_lysosomal_hyaluronidase/gb=aj000099/_ntype=rna
d83260_604-1150,hxc-26_mrna,_complete_cds
j04823mrna_61-391,cytochrome_c_oxidase_subunit_viii_(cox8)_mrna,_complete_cds_
l11066_2272-2770,mrna_sequence_
l13939_3297-3791,beta_adaptin_protein_mrna,_complete_cds_
35 l25878_1092-1657,p33/heh_epoxide_hydrolase_(ephx)_mrna,_complete_cds
m34668_3044-3590,protein_tyrosine_phosphatase_(ptpase-alpha)_mrna
m64929_1572-2100,protein_phosphatase_2a_alpha_subunit_mrna,_complete_cds_
m74491_3066-3552,adp-ribosylation_factormrna,_complete_cds
m88279_1591-2131,immunophilin_(fkbp52)_mrna,_complete_cds

m94046_1788-2346,zinc_finger_protein_(maz)_mrna
 s82470_1398-1836,_bb1=malignant_cell_expression-enhanced_gene/tumor_progression-enhanced_gene_[human
 u04241_979-1264,homolog_of_drosophila_enhancer_of_split_m9/m10_mrna,_complete_cds
5 u13991_335-713,tata-binding_protein_associated_factor_30_kda_subunit_(tafii30)_mrna,_complete_cds
 u18937_1840-2344,histidyl-tma_synthetase_homolog_(ho3)_mrna,_complete_cds_
 u32986_3609-4126,xeroderma_pigmentosum_group_e_uv-damaged_dna_binding_factor_mrna,_complete_cds
10 u37146_5411-5927,silencing_mediator_of_retinoid_and_thyroid_hormone_action_(smrt)_mrna,_complete_cds
 u41635_2207-2651,os-9_precurosor_mrna,_complete_cds
 u60644_1537-1957,hu-k4_mrna,_complete_cds
 u65579_138-648,mitochondrial_nadh_dehydrogenase-ubiquinone_fe-s_protein_8,_23_kda_subunit_precursor_
15 u67171_229-697,selenoprotein_w_(selw)_mrna,_complete_cds/gb=u67171_/ntype=rna
 u78735_5872-6424,abc3_mrna,_complete_cds
 u79287_813-1305,clone_23867_mrna_sequence
 u82108_987-1464,sip-1_mrna,_complete_cds_
20 u83246_1364-1904,copine_i_mrna,_complete_cds_
 u95040_2366-2876,transcriptional_corepressor_hkap1/tif1b_mrna,_complete_cds
 all_x04106_907-1478,mrna_for_calcium_dependent_protease_(small_subunit)
 x57346cds_308-674:in_reversesequence,_1118-1154,mrna_for_hs1_protein
 x70649_2231-2663,cl.1042_mrna_of_dead_box_protein_family_
25 all_x72964_606-1027,mrna_for_caltractin
 all_x73358_355-815,haes-1_mrna_
 x92896exon#2-3_39-222:in_reversesequence,_295-301,mrna_for_itba2_protein
 x98801cds_3489-3729:in_reversesequence,_3771-4017,mrna_for_dynactin_
 x99728exon_13-247,ndufv3_gene,_exon/gb=x99728_/ntype=dna/_annot=exon
30 y07604cds_291-483:in_reversesequence,_572-776,mrna_for_nucleoside-diphosphate_kinase_z14244cds_31-169:in_reversesequence,_43-
 409,coxviib_mrna_for_cytochrome_c_oxidase_subunit_viiib
 z56281cds_772-1222:in_reversesequence,_1334-1382,mrna_for_interferon_regulatory_factor_3
 all_z69881_3952-4535,mrna_for_adenosine_triphosphatase,_calcium

35

Metagene 207

hg2160-ht2230_at hg2160-ht2230_glutamate_decarboxylase
 u68723_2126-2576,checkpoint_suppressormrna,_complete_cds

x76059cds_1208-1424:in_reversesequence,_1709-1807,mrna_for_yrrm1

Metagene 206

- 5 m90354cds_29-301:in_reversesequence,_1165-1197,btf3_protein_homologue_gene,_complete_cds
u57452_43-103,snf1-like_protein_kinase_mrna,_partial_cds/gb=u57452_/ntype=rna
u62432_1759-
- 1881,nicotinic_acetylcholine_receptor_alpha3_subunit_precursor,_mrna,_complete_cds_
x87852cds_5374-5560:in_reversesequence,_5780-5966,mrna_for_sex_gene_
- 10 all_z29678_1247-1740,mitf_mrna_

Metagene 62

- u07132_1415-1961,steroid_hormone_receptor_ner-i_mrna,_complete_cds_
- 15 x99374cds_1846-2174:in_reversesequence,_2211-2318,mrna_for_fertilin_beta

Metagene 387

- ab002409_293-791,mrna_for_slc,_complete_cds/gb=ab002409_/ntype=rna
- 20 af009368_901-1345,luman_mrna,_complete_cds/gb=af009368_/ntype=rna_
- d11327_2099-2638,mrna_for_protein-tyrosine_phosphatase,_complete_cds_
- d16827cds_767-1064:in_reversesequence,_1124-
- 1132,gene_for_fifth_somatostatin_receptor_subtype_
- d17461exon#1-3_13-102:not_in_gb_record,gulo_gene_for_l-gulono-gamma-
- 25 lactone_oxidase,_exon_9,10_and/g
- d21089_2957-3515,mrna_for_xp-c_repair_complementing_protein_(p125),_complete_cds_
- d31891_3786-4275,mrna_for_kiaa0067_gene,_complete_cds
- d32002_2454-3001,mrna_for_nuclear_cap_binding_protein,_complete_cds
- d42053_3755-4277,mrna_for_kiaa0091_gene,_complete_cds
- 30 d50312_1206-1668,mrna_for_ukatp-1,_complete_cds
- d63485_2710-3196,mrna_for_kiaa0151_gene,_complete_cds
- d85939_746-1037,mrna_for_p97_homologous_protein,_complete_cds
- d87012cds_1986-2226:in_fullsequence,_34522-34687,(lambda)_dna_for_immunoglobulin_light_chain
- d87432_5731-6253,mrna_for_kiaa0245_gene,_complete_cds
- 35 d90279_5154-5590,mrna_for_collagen_alpha_1(v)_chain,_complete_cds
- hg2442-ht2538_at_hg2442-
- ht2538_tropomyosin,_alpha,_muscle,_altslice_2,_skeletal_muscle_(fibroblast)
- hg2686-hf2782_at_hg2686-hf2782_ryanodine_receptor_

hg2992-ht5186_at_hg2992-ht5186_beta-hexosaminidase,_alpha_polypeptide,_abnormal_splice_mutation
 hg3175-ht3352_at_hg3175-ht3352_carcinoembryonic_antigen
 hg3254-ht3431_at_hg3254-ht3431_phosphatidylinositol_3-kinase_p110,_beta_isoform
5 j00220_cds4_at_j00220_j00220,not_in_gb_record,ig_germline_h-chain_g-e-a_region_a:_gamma-3'_flank,i
 j02854_531-1089,20-kda_myosin_light_chain_(mlc-2)_mrna,_complete_cds_
 j03810_2627-3113,liver_glucose_transporter-like_protein_(glut2),_complete_cds
 all_k03430_414-853,complement_c1q_b-chain_gene_
10 l04751_1994-2510,cytochrome_p-450_4a_(cyp4a)_mrna,_complete_cds
 110378_1130-1640,(clone_ctg-b43a)_mrna_sequence
 110955cds#1_184-560:in_reversesequence,_394-
 467,_carbonic_anhydrase_iv_gene_extracted_fromcarbonic_a
 111369_756-1296,protocadherin_42_mrna,_3'_end_of_cds_for_alternative_splicing_pc42-8_
15 all_111672_3552-
 3579,kruppel_related_zinc_finger_protein_(htf10)_mrna,_complete_cds,kruppel_related_
 113329exon_434-938,iduronate-2-sulfatase_(ids)_gene_
 114565exon#9_5-359,peripherin_(prph)_gene_exons_1-9,_complete_cds
 115409_1227-1719,(clone_g7)_von_hippel-lindau_disease_tumor_suppressor_mrna_sequence
20 l20815_2031-2445,s_protein_mrna,_complete_cds
 l29376_616-1126,(clone_3.8-1)_mhc_i_mrna_fragment_
 l33930_1504-2054,cd24_signal_transducer_mrna,_complete_cds_and_3'_region
 l42324cds_530-944,(clone_gpcr_w)_g_protein-linked_receptor_gene_(gpcr)_gene,_5'_end_of_cds/gb=l42324
25 l42450mrna_1022-1448,pyruvate_dehydrogenase_kinase_isoenzyme(pdk1)_mrna,_complete_cds
 l47125mrna_1504-2055,(chromosome_x)_glypican_(gpc3)_mrna,_complete_cds
 l48211cds_31-151:in_reversesequence,_1691-1775,angiotensin_ii_receptor_gene,_complete_cds
 l49173cds_13-116,ocp2_gene,_partial_cds/gb=l49173/_ntype=dna/_annot=cds
 m14539_3238-3730,factor_xiii_subunit_a_mrna,_3'_end
30 m19507mrna#4_2620-3184,myeloperoxidase_mrna,_complete_cds
 m20778_401-974,_homo_sapien,_alpha-3_(vi)_collagen
 m20786exon_630-1146,alpha-2-plasmin_inhibitor_gene_
 all_m21494_152-645:in_m21494cds_888-967,muscle_creatine_kinase_gene_(ckmm),_5'_flank
 all_m22919_3226-3665,_mlc_gene_(non-
35 muscle_myosin_light_chain)_extracted_fromnonmuscle/smooth_muscle
 m37755exon_15-256:in_reversesequence,_280-453:not_in_gb_record,pregnancy-specific_beta-1-glycoprotei
 m58583_989-1487,precerebellin_and_cerebellin_mrna,_complete_cds
 m64347_3336-3720,novel_growth_factor_receptor_mrna,_3'_cds_

m74297_1161-1551,homeobox_1.4_protein_mrna,_complete_cds_
m75106_1138-1618,prepro-plasma_carboxypeptidase_b_mrna,_complete_cds_
m77810_2324-2585,transcription_factor_gata-2_(gata-2)_mrna,_complete_cds_
m82827mrna_2078-2228,fusion_protein_mrna,_complete_cds.

5 m91467_1375-1861,serotonin_receptor_(5ht1e)_mrna,_complete_cds_
m95929_1015-1399,homeobox_protein_(phox1)_mrna,_3'_end_
s76638_2553-3003,_p50-nf-
kappa_b_homolog_[human,_peripheral_blood_t_cells,_mrna,_3113_nt]
s82240_274-802,_rhoe=26_kda_gtpase_homolog_[human,_hela_cell_line,_mrna,_833_nt]

10 u03090_457-955,ca2+-dependent_phospholipase_a2_mrna,_complete_cds
all_u04325_3581-3780,_psg11_gene_(pregnancy-specific_beta-1-glycoproteinc-
a_domain)_extracted_frompr
u07969_2956-3259,intestinal_peptide-associated_transporter_hpt-1_mrna,_complete_cds
u08438exon#15_1106-1571,beta-adrenergic_receptor_kinase_(adrbk1)_gene

15 u17034_4182-4584,soluble_pla2_receptor_mrna,_complete_cds
u18550exon_1402-1954,gpr3_g_protein-coupled_receptor_gene,_complete_cds
u22961_2627-3194,mrna_clone_with_similarity_to_l-glycerol-3-
phosphate:nad_oxidoreductase_and_albumin
u24685cds_123-336:in_reversesequence,_420-447,anti-

20 b_cell_autoantibody_igm_heavy_chain_variable_v-d-
u40152_2541-3103,origin_recognition_complex(hsorc1)_mrna,_complete_cds
u55766_535-1081,rev_interacting_protein_rip-1_mrna,_complete_cds_
u64805_1668-2218,brca1-delta11b_(brca1)_mrna,_complete_cds/gb=u64805/_ntype=rna
u65011_1625-2039,preferentially_expressed_antigen_of_melanoma_(prame)_mrna,_complete_cds.

25 u69961_1565-1997,solurshin_(rgs)_mrna,_complete_cds
u70136_4546-4957,megakaryocyte_stimulating_factor_mrna,_complete_cds_
u71598_444-792,zinc_finger_protein_zfp2_(zf2)_mrna,_partial_cds
u88726_55-433,symplekin_mrna,_partial_cds/gb=u88726/_ntype=rna_
u90919_1637-2129,clones_23667_and_23775_zinc_finger_protein_mrna,_complete_cds_

30 all_x05276_1466-2031,mrna_for_fibroblast_tropomyosin_tm30_(pl)_
all_x05309_4846-5240,mrna_for_c3b/c4b_receptor_(cr1)_f_allotype
x14046cds_479-809:in_reversesequence,_944-1082,mrna_for_leukocyte_antigen_cd37
all_x14362_1961-2370,cr1_mrna_for_c3b/c4b_receptor_secuted_form_
x14675cds_31-163,bcr-abl_mrna_5'_fragment_(clone_3c)/gb=x14675/_ntype=rna

35 x55448exon#22_131-683,_g6pd_gene_(glucose-6-
phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
x61373mrna#1_3441-3693:not_in_gb_record,microtubule-
associated_protein_tau_(tau)_gene,_alternatively
all_x62078_1997-2400,mrna_for_gm2_activator_protein

x68264mrna_3300-
 3552,_muc18_gene_(melanoma_associated_glycoprotein)_extracted_frommgf_gene_exons_1&2
 x77567cds_853-1215:in_reversesequence,_1354-1518,mrna_for_insp3_5-phosphatase_
 all_x77753_2390-2787,trop-2_gene_

5 all_x83492_418-500,mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(4,7))/gb=x83492_/ntype=rna,mrna_for_fa
 x85740mrna_1112-1604,mrna_for_c-c_chemokine_receptor-4_
 x87211cds_486-1041,mrna_for_anion_exchange_protein/gb=x87211_/ntype=rna
 all_x90846_2935-3407,mrna_for_mixed_lineage_kinase_2,mrna_for_mixed_lineage_kinase_2

10 x97303mrna_11-93,mrna_for_ptg-12_protein/gb=x97303_/ntype=rna
 x98260cds_1280-1706,mrna_for_m-phase_phosphoprotein,_mpp11_
 y08134cds_1026-1362:in_reversesequence,_1531-1573,mrna_for_asm-like_phosphodiesterase_3b
 all_y08223_2471-2952,mfh-1_gene
 z11518mrna_1546-2066,mrna_for_histidyl-trna_synthetase_

15 z26256exon_64-364,isoformgene_for_l-
 type_calcium_channel,_exon/gb=z26256_/ntype=dna/_annot=exon

Metagene 482

20 l07515_253-790,heterochromatin_protein_homologue_(hp1)_mrna,_complete_cds
 l36051exon#6_678-1086,thrombopoietin_gene,_complete_cds
 u04811_1931-2375,trophinin_mrna,_complete_cds
 u09646exon_358-874,carnitine_palmitoyltransferase_ii_precursor_(cpt1)_gene_
 u11701_1316-1862,lim-homeobox_domain_protein_(hlh-2)_mrna,_complete_cds

25 u23946_1986-2496,putative_tumor_suppressor_(luca15)_mrna,_complete_cds_
 u42359mrna_1197-
 1217,n33_protein_form(n33)_gene,_exonand_complete_cds/gb=u42359_/ntype=dna/_annot=ex
 u49973cds#2_37-
 367,_orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtrigger1_transposab

30 u79263_995-1535,clone_23760_mrna,_partial_cds
 u86529_584-1130,glutathione_transferase_zeta(gstz1)_mrna,_complete_cds/gb=u86529_/ntype=rna_
 all_x52943_2163-2728,mrna_for_atf-a_transcription_factor_
 x98266cds#2_1028-1340:in_reversesequence,_2103-2223,_ligase-
 like_protein_gene_extracted_frommrna_for

35 z83802_133-511,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc3)

Metagene 358

hg2841-ht2970_at_hg2841-ht2970_albumin,_alts splice_5

u12259cds_492-808:in_reversesequence,_16275-16368,paired_box_homeotic_protein_(pax3)_gene
all_y07701_3290-3651,mrna_for_aminopeptidase_

Metagene 305

5

d17357exon_25-295,activin_beta-a_gene,_regulatory_sequence_of_5'_upstream_region/gb=d17357_/ntype=dna
d28124_1346-1886,mrna_for_unknown_product,_complete_cds
d86425_4224-4776,osteoblast_mrna_for_osteonidogen,_complete_cds
10 l12350mrna_5247-5721,thrombospondin(thbs2)_mrna,_complete_cds_
l13923_9109-9601,fibrillin_mrna,_complete_cds_
m12125mrna_671-1013,fibroblast_muscle-type_tropomyosin_mrna,_complete_cds
m83186_103-
316,cytochrome_c_oxidase_subunit_viiia_(cox7a)_muscle_isoform_mrna,_complete_cds_
15 m92934mrna_1492-2026,connective_tissue_growth_factor,_complete_cds_
u09278_2285-2735,fibroblast_activation_protein_mrna,_complete_cds
u19718_479-947,microfibril-associated_glycoprotein_(mfap2)_mrna,_complete_cds
u30521_1621-1951,p311_hum_-3.1_mrna,_complete_cds
u89942_2867-3383,lysyl_oxidase-related_protein_(ws9-14)_mrna,_complete_cds_
20 x02419mrna_1754-2210,upa_gene_
x57579exon_545-840:in_reversesequence,_1392-1555,activin_beta-a_subunit_(exon_2)
all_x63759_1241-1752,htnp2_gene_for_transition_protein_2_

Metagene 197

25

ab000114_1818-2208,mrna_for_osteomodulin,_complete_cds_
ab000905_1045-1253,dna_for_h4_histone,_complete_cds
af005043_3474-3990,poly(adp-ribose)_glycohydrolase_(hparg)_mrna,_complete_cds/gb=af005043_/ntype=rna
30 d42108_4054-4414,mrna_for_phospholipase,_complete_cds
d50927_3955-4411,mrna_for_kiaa0137_gene,_complete_cds
all_d87023_19383-19642,_j1_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_hg3231-ht3408_at_hg3231-ht3408_protease_receptor-1,_effector_cell
140384mrna_22-487,thyroid_receptor_interactor_(trip13)_mrna,_partial_cds/gb=l40384_/ntype=rna_
35 m60052_2004-2280,histidine-rich_calcium_binding_protein_(hrc)_mrna,_complete_cds_
m60315_2334-2838,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_
u09368_1908-2298,zinc_finger_protein_znf140
u36621exon_17-536,y-chromosome_rna_recognition_motif_protein_(yrrm)_gene
u47414_1449-1959,cyclin_g2_mrna,_complete_cds

u64198_3571-3955,il-12_receptor_beta2_mrna,_complete_cds_
y09443_1545-1935,mrna_for_alkyl-dihydroxyacetonephosphate_synthase_precursor_
all_z17240_956-1014,for_mrna_encoding_hmg2b_

5 Metagene 386

ab000584_618-1032,mrna_for_tgf-beta_superfamily_protein,_complete_cds
ab002366_5112-5616,mrna_for_kiaa0368_gene,_partial_cds/gb=ab002366/_ntype=rna
ab004884_2491-2995,mrna_for_pku-alpha,_partial_cds/gb=ab004884/_ntype=rna
10 d10995cds_828-1128:in_reversesequence,_1245-
1401,gene_for_serotonin_1b_receptor,_complete_cds_
d28588_2747-3263,mrna_for_kiaa0048_gene,_complete_cds
d63813_1154-1676,mrna_for_rod_photoreceptor_protein,_complete_cds
hg2730-ht2828_s_at_hg2730-ht2828_fibrinogen,_a_alpha_polyptide,_altslice_3,_e_
15 j05428_1624-1800,3,4-catechol_estrogen_udp-glucuronosyltransferase_mrna,_complete_cds
127080cds_538-946:in_reversesequence,_1159-
1207,melanocortinreceptor_(mc5r)_gene,_complete_cds_
m34192mrna_1406-1826,isovaleryl-coa_dehydrogenase_(ivd)_mrna,_complete_cds_
m37075_at_m37075_m37075,not_in_gb_record,embryonic/atrial_myosin_light_chain_(mlc-1-
20 emb/a_isoform)_g
m58285_3356-3788,membrane-associated_protein_(hem-1)_mrna,_complete_cds
m93143_461-499,plasminogen-like_protein_(plgl)_mrna,_complete_cds
m93415_1865-2303,activin_type_ii_receptor_mrna,_complete_cds_
m97496_25-409,guanylin_mrna,_complete_cds_
25 u03858_806-1040,flt3_ligand_mrna,_complete_cds
u09579_1537-2041,melanoma_differentiation_associated_(mda-6)_mrna,_complete_cds
u10690exon#3_934-1499,mage-5b_antigen_(mage5b)_gene,_complete_cds
u11863_1914-1974,clone_hp-
da02_diamine_oxidase,_copper/topa_quinoneContaining_mrna,_complete_cds
30 u15197_74-363,histo-blood_group_abo_protein_mrna,_partial_3'_utr_sequence
u17838_7401-7899,zinc_finger_protein_riz_mrna,_complete_cds
u55853_1917-2433,130_kd_golgi-localized_phosphoprotein_(gpp130)_mrna,_complete_cds
all_x83127_1494-1624,mrna_for_voltage_gated_potassium_channels,_beta_subunit_
x95654cds_2682-2862:in_reversesequence,_3022-3202,mrna_for_scpl_protein_
35 all_x98253_1221-1334,znf183_gene/gb=x98253/_ntype=rna

Metagene 294

a28102cds_986-1442:in_reversesequence,_1546-1582,gabaa_receptor_alpha-3_subunit.

m17446mrna_648-1186,kaposi_sarcoma_oncogene_fibroblast_growth_factor_mrna,_complete_cds
m98528utr#1_543-1101,neuron-specific_protein_gene,_last_exon,_clone_d4s234
u20816mrna#1_258-795,nuclear_factor_kappa-b2_(nf-
kb2)_gene,_partial_cds/gb=u20816/_ntype=dna/_annot=
5 all_u31799_528-683:in_u31799cds_1746-1777,melanocyte_protein_pmelgene_
all_x87870_2045-2289,mrna_for_hepatocyte_nuclear_factor_4a_

Metagene 238

10 m15856mrna#1_2984-3488,lipoprotein_lipase_mrna,_complete_cds_
m23575_1395-1933,pregnancy-specific_beta-1_glycoprotein_mrna,_complete_cds_
m60503cds_2942-3212:in_reversesequence,_1915-2047,profilaggrin_gene,_partial_cds
s81294_4-
160,_dcc=deleted_in_colorectal_cancer_{alternatively_spliced_exon_1a}_{[human,_brain_tumor,
15 all_s85963_4324-4544,_hirs-1=rat_insulin_receptor_substrate-
1_homolog_[human,_cell_line_focus,_genom

Metagene 200

20 m24351 exon_248-404,_pthlh_gene_(parathyroid_hormone-
like_protein_a)_extracted_fromparathyroid_hormon
m31210_2258-2708,endothelial_differentiation_protein_(edg-1)_gene_mrna,_complete_cds_
m55024_2-331,cell_surface_glycoprotein_p3.58_mrna,_partial_cds/gb=m55024/_ntype=rna
m58459_295-829,ribosomal_protein_(rps4y)_isoform_mrna,_complete_cds
25 m60626mrna_1283-1577,n-formylpeptide_receptor_(fmlp-r98)_mrna,_complete_cds
m60724_1847-2321,p70_ribosomal_s6_kinase_alpha-i_mrna,_complete_cds
s72024cds_13-437,_eif-
5a=eukaryotic_initiation_factor_5a_{clone_cos_9.1}_{[human,_placenta,_genomic,_
u13695cds_2418-2754:in_reversesequence,_2858-
30 2954,homolog_of_yeast_mutl_(hpms1)_gene,_complete_cds
u38896_1411-1921,zinc_finger_protein_c2h2-171_mrna,_complete_cds_
x59434mrna_631-1129,rohu_mrna_for_rhodanese
all_x71661_2263-2768,ergic-53_mrna_
all_x96586_2898-3343,mrna_for_fan_protein
35

Metagene 364

131573_1849-2347,sulfite_oxidase_mrna,_complete_cds
m11973_cds1_at_m11973_m11973,not_in_gb_record,gamma-b-crystallin_gene_(gamma_1-2)_

m29474mrna_5986-6490,recombination_activating_protein_(rag-1)_gene,_complete_cds_
 u08471_492-780,folate_receptor_mrna,_complete_cds
 u57352_2094-2646,sodium_channel(hbnac1)_mrna,_complete_cds
 u76388_1630-1842,steroidogenic_factor_mrna,_complete_cds_
5 all_z22536_1732-2333,alk-4_mrna,_complete_cds_

Metagene 343

d25217_2864-3410,mrna_for_kiaa0027_gene,_partial_cds_
10 d45371mrna_4040-4464,apm1_mrna_for_gs3109_(novel_adipose_specific_collagen-like_factor),_complete_cd
 d85815cds_282-564,in_reversesequence,_753-879,dna_for_rhohp1,_complete_cds
 hg1205-ht1205_at_hg1205-ht1205_collagen,_type_iv,_alpha_2,_n-terminus
 hg4157-ht4427_at_hg4157-ht4427_glycinamide_ribonucleotide_synthetase_
15 hg732-ht732_at_hg732-ht732_serum_amyloid_a1
 j03600_2058-2364,lipooxygenase_mrna,_complete_cds_
 k01911mrna_85-481,neuropeptide_y_(npy)_mrna,_complete_cds
 l05148_1890-2388,protein_tyrosine_kinase_related_mrna_sequence_
 l05779_1535-2069,cytosolic_epoxide_hydrolase_mrna,_complete_cds
20 l10123_3572-4100,surfactant_protein_a_mrna,_complete_cds
 l19297_602-1034,nuclear-encoded_mitochondrial_carbonic_anhydrase_(ca5)_mrna,_complete_cds
 l29277_2204-2762,dna-binding_protein_(aprfl)_mrna,_complete_cds
 l38707mrna_2405-2951,diacylglycerol_kinase_(dagk)_mrna,_complete_cds.
 l41668_887-1433,udp-galactoseepimerase_(gale)_gene,_complete_cds
25 l48516_473-1013,paraoxonase(pon3)_mrna,_3'_end_of_cds
 m13829_603-1029,putative Raf_related_protein_(pks/a-raf)_mrna,_partial_cds_
 m14565mrna_1262-1712,cholesterol_side-chain_cleavage_enzyme_p450scc_mrna,_complete_cds_
 m20777_434-956,homo_sapiens,_alpha-2_(vi)_collagen_
 m29696_1063-1597,interleukin-7_receptor_(il-7)_mrna,_complete_cds
30 m37271cds_361-672,in_reversesequence,_2722-2909,cd7_antigen_gene,_exons_4-jan_
 m54951mrna_438-852,atrial_natriuretic_factor_gene
 all_m59829_2774-3117,mhc_iii_hsp70-hom_gene_(hla),_complete_cds
 m60298_2117-2615,erythrocyte_membrane_protein_band_4.2_(epb42)_mrna,_complete_cds
 m68519mrna_1542-1916,pulmonary_surfactant-associated_protein_sp-
35 a_(sf1p1)_gene,_complete_cds
 m69197mrna#1_611-1184,_hpr_fromhaptoglobin_and_haptoglobin-related_protein_(hp_and_hpr)_genes,_compl
 m74091_925-1453,cyclin_mrna
 m80629_1678-2170,cdc2-related_protein_kinase_(ched)_mrna,_complete_cds_

m89957_675-
 1095,immunoglobulin_superfamily_member_b_cell_receptor_complex_cell_surface_glycoprotein_
 m93405_888-1374,methylmalonate_semaldehyde_dehydrogenase_gene,_complete_cds_
 m93650_1119-1599,paired_box_gene_(pax6)_homologue,_complete_cds
5 m99701_627-1137,(pp21)_mrna,_complete_cds_
 s69265_1402-1943,_neuron-specific_rna_recognition_motifs_(rrms)-
 containing_protein_[human,_hippocamp
 s75989_1492-1948,_gamma-
 aminobutyric_acid_transporter_type[human,_fetal_brain,_mrna,_1991_nt]
10 s76475_2144-2659,_trkc_[human,_brain,_mrna,_2715_nt]
 u07358_2794-3310,protein_kinase_(zpk)_mrna,_complete_cds_
 u09877_3381-3849,helicase-like_protein_(hlp)_mrna,_complete_cds
 u10991_6267-6789,g2_protein_mrna,_partial_cds
 u16031_2451-2943,transcription_factor_il-4_stat_mrna,_complete_cds_
15 u26398_2628-3168,inositol_polyphosphate_4-phosphatase_mrna,_complete_cds_
 u26403_991-1495,receptor_tyrosine_kinase_ligand_lerk-7_precursor_(eplg7)_mrna,_complete_cds
 u30930_1877-2423,udp-galactose_ceramide_galactosyl_transferase_(cgt)_mrna,_complete_cds
 u43431_3166-3712,dna_topoisomerase_iii_mrna,_complete_cds
 u52840_7503-7755,cri-du-chat_region_mrna,_clone_csa1_
20 u64998cds_61-
 361,ribonuclease_k6_precursor_gene,_complete_cds/gb=u64998/_ntype=dna/_annot=cds
 u82535_1485-2019,fatty_acid_amide_hydrolase_mrna,_complete_cds.
 all_v00565_2218-
 2422,gene_for_preproinsulin,_from_chromosomeincludes_a_highly_polymorphic_region_ups
25 x04445mrna_521-1075,inha_gene_exon(and_joined_cds)
 x06985mrna_943-1393,mrna_for_heme_oxygenase
 x07732mrna#2_991-1543,hepatoma_mrna_for_serine_protease_hepsin_
 all_x52773_1343-1866,mrna_for_retinoic_acid_receptor-like_protein
 x60188mrna_1360-1741,erk1_mrna_for_protein_serine/threonine_kinase_
30 x60957cds_3066-3378,in_reversesequence,_3432-
 3678,tie_mrna_for_putative_receptor_tyrosine_kinase_
 x86779cds_1174-1606,in_reversesequence,_1741,mrna_for_fast_kinase_
 x99961cds_55-409,mrna_for_novel_protein/gb=x99961/_ntype=rna_
 z26317cds_2904-3324,in_reversesequence,_3443-3491,mrna_for_desmoglein_2_
35

Metagene 174

d89289_1431-1947,mrna_for_n-acetyl-beta-d-glucosaminide,_complete_cds

105188cds_2-194:in_reversesequence,_281-342,small_proline-rich_protein(sprn2b)_gene,_complete_cds_m74509_7730-8246,endogenous_retrovirus_type_c_oncovirus_sequence.
 5 s70004_2347-2779,_glycogen_synthase_[human,_liver,_mrna,_2912_nt]_u65416mrna_1983-2316,mhc_i_molecule_(micb)_gene,_complete_cds_u79285_892-1402,clone_23828_mrna_sequence

Metagene 171

10 hg1111-ht1111_at_hg1111-ht1111_ras-like_protein_tc21_k02100mrna_983-1421,ornithine_transcarbamylase_(otc)_mrna,_complete_coding_sequence
 u08015mrna_2388-2700,nf-atc_mrna,_complete_cds_u09413_1957-2389,zinc_finger_protein_znf135_mrna,_complete_cds_u70862_1029-1248,nuclear_factor_i_b3_mrna,_complete_cds
 15 all_x01059_941-1512,placenta_mrna_for_luteinizing_hormone_releasing_hormone_precursor_(lhrh)_all_x66436_1427-1980,hsrl1_mrna_(partial)_x80507cds_1020-1314:in_reversesequence,_1624-1828,yap65_mrna_all_x99141_1411-1715,mrna_for_hair_keratin,_hhb3_

20

Metagene 51

d13988_897-1353,rab_gdi_mrna,_complete_cds_d31763_5458-5968,mrna_for_kiaa0065_gene,_partial_cds
 25 hg1747-ht1764_s_at_hg1747-ht1764_proto-oncogene_met,_altslice_form_2 hg4074-ht4344_at_hg4074-ht4344_rad2 j05614mrna_4-41,proliferating_cell_nuclear_antigen_(pcna)_gene,_promoter_region/gb=j05614_/ntype=dna
 i23959_971-1415,e2f-related_transcription_factor_(dp-1)_mrna,_complete_cds
 30 140386mrna_657-1122,dp-2_mrna,_complete_cds 140403mrna_1725-2277,(clone_zap3)_mrna,_3'_end_of_cds_m28209_158-680,gtp-binding_protein_(rab1)_mrna,_complete_cds
 m37104_13-421,mitochondrial_atpase_coupling_factorsubunit_(atp5a)_mrna,_complete_cds
 m37583mrna_368-824,histone_(h2a.z)_mrna,_complete_cds
 35 m58525_603-933,catechol-o-methyltransferase_(comt)_mrna,_complete_cds_m81118exon#2_669-1149,alcohol_dehydrogenase_chi_polypeptide_(adh5)_gene
 m83738_3328-3883,protein-tyrosine_phosphatase_(ptpase_meg2)_mrna,_complete_cds_m86737_2236-2776,high_mobility_group_box_(ssrp1)_mrna,_complete_cds
 m92439_4255-4633,leucine-rich_protein_mrna,_complete_cds

m94630_832-1027,hnrrnp-c_like_protein_mrna,_complete_cds_
 s83364_19-325,_putative_rab5-interacting_protein_{clone_11-
 57}_{[human,_hela_cells,_mrna_partial,_366
 s85655_435-969,_prohibitin_[human,_mrna,_1043_nt]}
5 u25182_350-860,antioxidant_enzyme_aoe37-2_mrna,_complete_cds_
 u41387_2693-3263,gu_protein_mrna,_partial_cds
 u56833_940-1468,vhl_binding_protein-1_(vbp-1)_mrna,_partial_cds
 u57627_4598-5078,fetal_brain_oculocerebrorenal_syndrome_(ocrl1)_mrna,_complete_cds_
 u65410_961-1459,mad2_(hsmad2)_mrna,_complete_cds_
10 u83843_725-1145,hiv-1_nef_interacting_protein_(nip7-1)_mrna,_partial_cds/gb=u83843_/ntype=rna
 all_x92396_1999-2480,mrna_for_novel_gene_in_xq28_region
 x94754cds_2213-2645:in_reversesequence,_2712-2730,mrna_for_yeast_methionyl-
 tRNA_synthetase_homologue
 all_x99585_193-608,mrna_for_smt3b_protein
15

Metagene 19

hg721-ht4827_s_at_hg721-ht4827_placental_protein_14,_endometrial_alpha1globulin,_alts splice_2_
 119593mrna_2261-2747:in_reversesequence,_2765-
20 2771,interleukinreceptor_beta_(il8rb)_mrna,_complete_c
 s34389_1166-1586,_heme_oxygenase-2_[human,_kidney,_mrna,_1627_nt]
 u19523_2299-2851,gtp_cyclohydrolase_i_mrna,_complete_cds
 all_x05232_1530-1771,mrna_for_stromelysin
 x12662mrna_936-1398,arginase_gene_exonand_flanking_regions_(ec_3.5.3.1)_(and_joined_cds)
25 all_x57809_309-
 474,rearranged_immunoglobulin_lambda_light_chain_mrna,rearranged_immunoglobulin_lambd
 x72308_419-842,mcp-3_mrna_for_monocyte_chemotactic_protein-3_
 y00081cds_293-588:in_reversesequence,_5486-5706,(bsf-
 2/il6)_gene_for_b_cell_stimulatory_factor-2
30 y11306mrna_1993-2395,_htcf-4_gene_extracted_frommrna_for_beta_catenin/tcf-4

Metagene 370

l20971_3698-3992,phosphodiesterase_mrna,_complete_cds
35 u03272_9619-10081,fibrillin-2_mrna,_complete_cds_
 u07802exon#2_2748-3228,tis11d_gene,_complete_cds_
 all_x78565_6971-7512,mrna_for_tenascin-c,_7560bp_

Metagene 312

d31716_4264-4831,mrna_for_gc_box_bindig_protein,_complete_cds
 114430_at_114430_114430,not_in_gb_record,udp-
 glucose_pyrophosphorylase_mrna,_complete_cds_and_flanki
5 u26591_1640-
 2108,clone_is10_diabetes_mellitus_type_i_autoantigen_(icap69)_mrna,_complete_cds_
 u33837_13803-14343,glycoprotein_receptor_gp330_precursor,_mrna,_complete_cds_
 u33880mrna_189-
 240,betaintegrin_isoform_d_(itgb1)_gene,_partial_cds/gb=u33880/_ntype=dna/_annot=exon
10 u62434_1665-
 1787,nicotinic_acetylcholine_receptor_alpha5_subunit_precursor,_mrna,_complete_cds_
 all_x56199_1025-1614,xist,_coding_sequence_a_mrna_(locus_dx399e)
 x60382mrna_2717-3149,col10a1_gene_for_collagen_(alpha-1_type_x)_
 z48520exon#5_1-98:in_reversesequence,_154-163,xg_mrna_(clone_race6)/gb=z48520/_ntype=rna
15
 Metagene 114

 hg3928-ht4198_s_at_hg3928-ht4198_surfacant_protein_sp-a1_delta_
 105597cds_729-1071:in_reversesequence,_1307-1499,serotonin_receptor_gene,_complete_cds
20 u76189_49-355,extl3_mrna,_partial_cds/gb=u76189/_ntype=rna

 Metagene 110

 d13705_1151-1722,mrna_for_fatty_acids_omega-hydroxylase_(cytochrome_p-
25 450hkv),_complete_cds
 d16105_2703-2979,mrna_for_leukocyte_tyrosine_kinase,_complete_cds
 d83017_2365-2810,mrna_for_nel-related_protein,_complete_cds
 hg2255-ht2344_f_at_hg2255-ht2344_phosphoribosyl_pyrophosphate_synthetase,_subunit_iii
 hg2797-ht2906_s_at_hg2797-ht2906_clathrin,_light_polypeptide_alts splice_2
30 k03192_566-964,cytochrome_p-450_mrna,_partial
 m13058exon#3_1-372,acidic_proline-rich_protein_(prh2)_gene,_complete_cds_
 m13149_1540-2008,histidine-rich_glycoprotein_mrna,_complete_cds
 all_m29335_62-94,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-alpha_mrna,_partial_cds
 all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-
35 hydroxylase_(cyp11b1)
 m33772mrna_69-631,fast_skeletal_muscle_troponin_c_gene_
 m55513mrna_2274-2767,potassium_channel_(hpcn1)_mrna,_complete_cds
 m62303_726-872,retinoic_acid_receptor-beta_associated_open_reading_frame,_complete_sequence
 m64269cds_389-718:in_reversesequence,_7859-7876,mast_cell_chymase_gene,_complete_cds

m74587mrna_953-1425,insulin-like_growth_factor_binding_protein_(higfbp1)_gene,_complete_cds_m83652_932-1457,complement_component_properdin_mrna,_complete_cds_s77576_3-

5 60,_erv9_reverse_transcriptase_homolog_{clone_rt18}_[human_multiple_sclerosis_brain_plaque] u05012_2204-2720,receptor_tyrosine_kinase_trkc_(ntrk3)_mrna,_complete_cds u11862_1844-2402,clone_hp-dao1_diamine_oxidase,_copper/topa_quinone-containing_mrna,_complete_cds u12140_3433-3673,tyrosine_kinase_receptor_p145trk-b_(trk-b)_mrna,_complete_cds

10 u23850_8177-8697,inositol_1,4,5_trisphosphate_receptor_typemrna,_partial_cds u24488_2519-3042,tenascin-x_(xa)_mrna,_complete_cds u25771_1383-1821,adp-ribosylation_factor_mrna,_complete_cds u52373_1810-2355,serine/threonine_kinase_mnb_(mnb)_mrna,_complete_cds u57623exon#1-4_51-

15 240:in_reversesequence,_6798,fatty_acid_binding_protein_fabp_gene,_complete_cds_u80034_1785- 2283,mitochondrial_intermediate_peptidase_precursor_(mipep)_mrna,_mitochondrial_gene_enc u81599_751-1273,homeodomain_protein_hoxb13_mrna,_complete_cds u86214_1736-2000,fas-associated_death_domain_protein_interleukin-1b-converting_enzymemrna,_complete_

20 u88898_561-757,endogenous_retroviral_h_protease/integrase-derived_orf1_mrna,_complete_cds,_and_putat all_x07618_880-1388,mrna_for_cytochrome_p450_db1_variant_a_ all_x07730_1535-1680,mrna_for_prostate_specific_antigen

25 all_x14253_1410-2003,mrna_for_cripto_protein_ all_x66867_1864-2066:in_x66867cds#2_310,_max_gene_extracted_frommax_gene_x94628mrna_952-1510,mecp-2_gene_ x99688_3790-4270,mrna_from_tyl_gene all_y08613_599-1164,alternative_3'_utr_of_nup88_mrna/gb=y08613_/ntype=rna

30 z35227cds_385-547:in_reversesequence,_1162-1318,ttf_mrna_for_small_g_protein

Metagene 98

ab002559_1302-1746,mrna_for_hunc18b2,_complete_cds_af006087_237-777,arp2/3_protein_complex_subunit_p20-arc_(arc20)_mrna,_complete_cds/gb=af006087_/ntyp d10511cds_860-1256:in_reversesequence,_165-243,gene_for_mitochondrial_acetoacetyl-coa_thiolase d26308_241-691,mrna_for_nadph-flavin_reductase,_complete_cds_

d26598_187-571,mrna_for_proteasome_subunit_hsc10-ii,_complete_cds
d31764_1478-1982,mrna_for_kiaa0064_gene,_complete_cds
d38047_327-825,mrna_for_26s_proteasome_subunit_p31,_complete_cds_
d38751_1539-1868:not_in_gb_record,mrna_for_kid_(kinesin-
5 like_dna_binding_protein),_complete_cds_
d43947_6379-6901,mrna_for_kiaa0100_gene,_complete_cds
d50645_502-1006,mrna_for_sdf2,_complete_cds
d85433_109-439,murr1_mrna,_sequence/gb=d85433_/ntype=rna_
hg3638-ht3849_s_at_hg3638-ht3849_amyloid_beta_(a4)_precursor_protein,_altslice_2,_a4(751)_
10 j04444cds_596-944:in_reversesequence,_3590-3740,cytochrome_c-1_gene,_complete_cds_
l20320cds_605-
953:in_reversesequence,_1218,protein_serine/threonine_kinase_stk1_mrna,_complete_cds
137042mrna_960-1314,casein_kinase_i_alpha_isoform_(csnk1a1)_mrna,_complete_cds
140410mrna_296-803,thyroid_receptor_interactor_(trip3)_mrna,_3'_end_of_cds
15 l41559mrna_61-475,pterin-4a-carbinolamine_dehydratase_(pcbd)_mrna,_complete_cds_
m15661mrna_3-338,ribosomal_protein_mrna,_complete_cds
m19483cds_1127-1559:in_reversesequence,_2162-2204,atp_synthase_beta_subunit_gene
m29971_282-750,6-o-methylguanine-dna_methyltransferase_(mgmt)_mrna,_complete_cds_
m55153_2794-3232,transglutaminase_(tgase)_mrna,_complete_cds_
20 u34343_110-560,13kd_differentiation-associated_protein_mrna,_partial_cds/gb=u34343_/ntype=rna
u43923_888-1410,transcription_factor_supt4h_mrna,_complete_cds_
u65093_466-838,msg1-related_gene(mrg1)_mrna,_complete_cds_
u79262_878-1007,deoxyhypusine_synthase_mrna,_complete_cds
u79718_532-1012,endonuclease_iii_homolog(octs3)_mrna,_complete_cds
25 all_x90857_2739-3184,mrna_for_-14_gene,_containing_globin_regulatory_element_
x94910_333-861:not_in_gb_record,mrna_for_erp31_protein
y08766cds_1803-1893:in_reversesequence,_2190-2239,mrna_for_splicing_factor,_sf1-bo_isoform
y12478_210-750,mrna_for_chd5_protein_

30 Metagene 464

d16593_290-812,bdr-2_mrna_for_hippocalcin,_complete_cds
d88460_1233-1695,mrna_for_n-wasp,_complete_cds_
d89016_1618-2116,mrna_for_neuroblastoma,_complete_cds
35 hg2280-ht2376_at_hg2280-ht2376_d-amino-acid_oxidase
hg908-ht908_at_hg908-ht908_mg61_protein
100635_1029-1437,farnesyl-protein_transferase_beta-subunit_mrna,_complete_cds
134355_827-961,(clone_p4)_50_kd_dystrophin-associated_glycoprotein_mrna,_complete_cds_
136818_4098-4608,(clone_51c-3)_51c_protein_mrna,_complete_cds

144140exon#61-62_44-

221:not_in_gb_record_dn111_gene_extracted_fromchromosome_x_region_from_filamin_m38258_2000-2486,retinoic_acid_receptor_gammamrna,_complete_cds_m77348mrna_1757-1786,pmelmrna,_complete_cds_

5 m92432_3098-3566,retinal_guanylyl_cyclase_(retgc)_mrna,_complete_cds_m96759mrna_783-1299,rod_outer_segment_membrane_protein(rom1)_gene_exons_1-3,_complete_cds_all_s58733_264-

357_pp52=b_lymphocyte_signal_transduction_gene_{group_3,inverted_repeat}_*[human,tu

10 u07418_2004-2454,dna_mismatch_repair_(hmlh1)_mrna,_complete_cds_u37529_556-1030,substance_p_beta-ppt-a_mrna,_complete_cds_u43177exon#1_62-464,urocortin_gene,_complete_cds_u49928_2513-3035,tak1_binding_protein(tab1)_mrna,_complete_cds_u62966_2137-2635,na+/nucleoside_cotransporter_(hcnt1a)_mrna,_complete_cds

15 u68536_1918-2410,zinc_finger_protein_mrna,_complete_cds_u71087_1092-1126,map_kinase_kinase_mek5b_mrna,_complete_cds_u92314_840-1415,hydroxysteroid_sulfotransferase_sult2b1a_(hsst2)_mrna,_complete_cds.all_x06256_3681-4180,mrna_for_fibronectin_receptor_alpha_subunit_all_x13589_2395-2936,mrna_for_aromatase_(estrogen_synthetase)

20 all_x54871_1059-1612,mrna_for_ras-related_protein_rab5b_all_x86681_1848-2257,mrna_for_nucleolar_protein_hnp36_all_x94453_2396-2907,mrna_for_pyroline_5-carboxylate_synthetase_

Metagene 360

25 d28137_395-743,mrna_for_bst-2,_complete_cds_j04164_366-804,interferon-inducible_protein_27-sep_mrna,_complete_cds_l22342_672-810,nuclear_phosphoprotein_mrna,_complete_cds_m13755mrna_33-591,interferon-induced_17-kda/15-kda_protein_mrna,_complete_cds

30 m31724mrna_2694-3168,phosphotyrosyl-protein_phosphatase_(ptp-1b)_mrna,_complete_cds_m62505_1952-2240,c5a_anaphylatoxin_receptor_mrna,_complete_cds_u12255_905-1391,igg_fc_receptor_hfcrn_mrna,_complete_cds_u50648mrna_2211-2751,interferon-inducible_rna-dependent_protein_kinase_(pk)_gene_u72882_448-1009,interferon-induced_leucine_zipper_protein_(ifp35)_mrna,_partial_cds

35 u95006_114-654,d9_splice_variant_a_mrna,_complete_cds_x00371mrna_495-1011,myoglobin_gene_(exon_1)_and_joined_cds_all_x02874_1063-1298,mrna_for_(2'-5')_oligo_a_synthetase_e_(1,6_kb_rna) all_x02875_158-628,mrna_(3'_-fragment)_for_(2'_-5')_oligo_a_synthetase_e_(1,8_kb_rna)

all_x57351_294-891,1-8d_gene_from_interferon-inducible_gene_family,1-
8d_gene_from_interferon-inducib
x79882cds_2116-2656:in_reversesequence,_2773,lp_mrna_
x85116_rna1_s_at_x85116_x85116,not_in_gb_record,epb72_gene_exon_1_

5

Metagene 335

k02882cds_660-1098,_ighd_gene_(immunoglobulin_delta-
chain)_extracted_fromgermline_igd_chain_gene,_c-
10 m61199_1227-1689,cleavage_signalprotein_mrna,_complete_cds

Metagene 328

d25274_727-1177,randomly_sequenced_mrna
15 d49396_948-1446,mrna_for_apo1(mer5(aop1-mouse)-like_protein),_complete_cds
104731_13654-14152,translocation_t(4;11)_of_all-1_gene_to_chromosome_4
125081_595-1015,gtpase_(rhoc)_mrna,_complete_cds
m22538_286-778,nuclear-encoded_mitochondrial_nadh-
ubiquinone_reductase_24kd_subunit_mrna,_complete_c
20 m31951exon#2_671-1061:in_reversesequence,_6169,perforin_(prf1)_gene,_complete_cds
m63138mrna_1545-2007,cathepsin_d_(catd)_gene
s65738_1061-1373,_actin_depolymerizing_factor_[human,_fetal_brain,_mrna,_1452_nt]
u09848_2904-3474,zinc_finger_protein_(znf139)_mrna,_partial_cds
u43901mrna#1_429-
25 557,37_kd_laminin_receptor_precursor/p40_ribosome_associated_protein_gene,_complete
u83908cds_941-1295:in_reversesequence,_1589-1649,nuclear_antigen_h731_mrna,_complete_cds
u90878_693-1179,lim_domain_protein_clp-36_mrna,_complete_cds.
u90902_939-1407,clone_23612_mrna_sequence
u94855_696-1176,translation_initiation_factor47_kda_subunit_mrna,_complete_cds
30 all_x16416_4998-5497,c-abl_mrna_encoding_p150_protein
all_x51466_2702-3057,mrna_for_elongation_factor_2
x70218_771-1203,_hsapiens_mrna_for_protein_phosphatase_x
all_x74929_1365-1706,krt8_mrna_for_keratin_8_
all_x76228_677-1242,mrna_for_vacuolar_h+_atpase_e_subunit
35 x78136cds_688-1060:in_reversesequence,_1130-1244,hnrnp-e2_mrna
x82207cds_876-1098:in_reversesequence,_1166-1412,mrna_for_beta-centractin_(pc3)
y08999cds_583-1045:in_reversesequence,_1132,mrna_for_sop2p-like_protein_
all_z14000_958-1463,ring1_gene_
all_z49835_1354-1805,mrna_for_protein_disulfide_isomerase

Metagene 213

hg4321-ht4591_at_hg4321-ht4591_ahnak-related_sequence
5 j04449_2290-2776,(clone_nf_10)_cytochrome_p-450_nifedipine_oxidase_mrna,_complete_cds_
j05459mrna_695-1187,glutathione_transferase_m3_(gstm3)_mrna,_complete_cds_
117325_73-451,pre-t/nk_cell_associated_protein_(1d12a2)_mrna,_complete_cds_
l32164_630-1158,zinc_finger_protein_mrna,_3'_end
m16714exon#8_627-747,mhc_i_divergent_lymphocyte_antigen_gene,_complete_cds,_clone_rs5
10 all_m37457_334-371,na+,k+,#name?_catalytic_subunit_alpha-
iii_isoform_gene,na+,k+,#name?_catalytic_su
all_m86808_2578-2977,pyruvate_dehydrogenase_complex_(pdha2)_gene,_complete_cds_
all_x58723_1862-2049,mdr1_(multidrug_resistance)_gene_for_p-glycoprotein_
x92368mrna_5695-6187,ncx1_gene_(exon_1)/gb=x92368/_ntype=dna/_annot=mrna_

15

Metagene 92

d14826_834-1163,mrna_for_hcrem_(cyclic_amp-
responsive_element_modulator)_typeprotein,_complete_cds
20 hg2591-ht2687_s_at_hg2591-ht2687_transcription_factor_itf-1
u13696cds_2138-2563:in_reversesequence,_2600-
2669,homolog_of_yeast_mutl_(hpms2)_gene,_complete_cds
u60269cds#3_237-447:in_reversesequence,_1593-1737,endogenous_retrovirus_herv-
k(hml6)_proviral_clone_
25 x84740mrna_2847-3309,mrna_for_dna_ligase_iii_
y10275cds_363-633:in_reversesequence,_880-1060,mrna_for_l-3-phosphoserine_phosphatase_

Metagene 64

30 hg2702-ht2798_r_at_hg2702-ht2798_serine/threonine_kinase_
s79781mrna_31-
169,_wt1_{antisense_promoter,_intron_1}_[human,_kidney,_genomic,_780_nt]/gb=s79781/_nt
x54162mrna_3362-3818,mrna_for_a_64_kd_autoantigen_expressed_in_thyroid_and_extra-
ocular_muscle_
35 x61118mrna_1457-1955,_ttg-2a_gene_extracted_fromttg-
2_mrna_for_a_cysteine_rich_protein_with_lim_motif
y13896_4-179,skeletal_muscle_alternate_5'_end_of_gene_kir4.2_5'_utr/gb=y13896/_ntype=rna

Metagene 45

d38163_3117-3661,mrna_for_a1(xix)_collagen_chain,_complete_cds_
 all_x03066_787-1268,mrna_for_hla-d_ii_antigen_do_beta_chain
 x14766mrna_1363-1711,mrna_for_gaba-a_receptor,_alphasubunit_
5 x76104cds_4113-4257:in_reversesequence,_4629-4827,dap-kinase_mrna_
 z34974cds_1816-2144:in_reversesequence,_2439-2515,mrna_for_plakophilin_(partial)

Metagene 447

10 af006084_935-1277,arp2/3_protein_complex_subunit_p41-
 arc_(arc41)_mrna,_complete_cds/gb=af006084_/nty
 d00017_851-1319,lipocortin_ii_mrna_
 d26129_1145-1577,mrna_for_ribonuclease_a_(rnase_a),_complete_cds_
 d42043_2329-2863,mrna_for_kiaa0084_gene,_partial_cds_
15 d87292_572-1052,mrna_for_rhodanese,_complete_cds_
 d88152_2081-2639,mrna_for_acetyl-coenzyme_a_transporter,_complete_cds
 j04456_31-469,_humankd_lectin_mrna,_complete_cds
 l13720_1860-2436,growth-arrest-specific_protein_(gas)_mrna,_complete_cds
 l25080_1212-1692,gtp-binding_protein_(rhoa)_mrna,_complete_cds_
20 l33075_6978-7530,ras_gtpase-activating-like_protein_(iqgap1)_mrna,_complete_cds_
 140379mrna_181-541,thyroid_receptor_interactor_(trip10)_mrna,_3'_end_of_cds_
 141147mrna_1383-1959,5-ht6_serotonin_receptor_mrna,_complete_cds
 m13450_636-1020,esterase_d_mrna,_3'_end
 all_m14338_2740-3281,mrna_for_protein_s_and_intron_
25 all_m14949_1905-2423,r-ras_gene
 m23294mrna#1_1219-1651,beta-hexosaminidase_beta-subunit_(hexb)_gene
 m26576exon_43-289:not_in_gb_record,_col4a1_gene_(alpha-
 1_type_iv_collagen)_extracted_fromalpha-1_col
 m27492_4336-4864,interleukinreceptor_mrna,_complete_cds_
30 m28713exon_536-1052,nadh-cytochrome_b5_reductase_(b5r)_gene_
 m33680_879-1431,26-kda_cell_surface_protein_tapa-1_mrna,_complete_cds
 m36341_912-1458,adp-ribosylation_factor(arf4)_mrna,_complete_cds
 m63256_1975-2497,major_yo_paraneoplastic_antigen_(cdr2)_mrna,_3'_end_
 m64571mrna_4553-4931,microtubule-associated_proteinmrna,_complete_cds_
35 m76378mrna_1294-1768,cysteine-rich_protein_(crp)_gene
 m82809_1465-1915,annexin_iv_(anx4)_mrna,_complete_cds
 m83751_539-1013,arginine-rich_protein_(arp)_gene,_complete_cds_
 u01691mrna_1257-1743,annexin_v_(anx5)_gene,_5'_untranslated_region
 u02570_2792-3290,cdc42_gtpase-activating_protein_mrna,_partial_cds_

u44378_2091-
 2655,homozygous_deletion_target_in_pancreatic_carcinoma_(dpc4)_mrna,_complete_cds
 u46006_140-620,smooth_muscle_lim_protein_(h-
 smlim)_mrna,_complete_cds/gb=u46006_/ntype=rna

5 u46499_at_u46499_u46499,not_in_gb_record,microsomal_glutathione_transferase_(gst12)_gene,_5'
 _sequenc
 u93205_588-1020,nuclear_chloride_ion_channel_protein_(ncc27)_mrna,_complete_cds
 x04412cds_2047-2305:in_reversesequence,_2421-2529,mrna_for_plasma_gelsolin
 all_x05610_1701-2098,mrna_for_type_iv_collagen_alpha_-2_chain

10 all_x07979_3223-3596,mrna_for_fibronectin_receptor_beta_subunit
 all_x54304_391-878,mrna_for_myosin_regulatory_light_chain
 y00433cds_233-581:in_reversesequence,_905-
 1109,mrna_for_glutathione_peroxidase_(ec_1.11.1.9.)

15 Metagene 70
 u02687_2874-3312,growth_factor_receptor_tyrosine_kinase_(stk-1)_mrna,_complete_cds_
 u79271_596-1130,clones_23920_and_23921_mrna_sequence_

20 Metagene 191
 hg3415-ht3598_at_hg3415-ht3598_poliovirus_receptor_
 j00124exon#8_14-227:not_in_gb_record,50_kda_type_i_epidermal_keratin_gene,_complete_cds
 all_100205_358-503,k6b_(epidermal_keratin,_type_ii)_gene_

25 l35594mrna_3002-3178,autotaxin_mrna,_complete_cds
 l42611_1374-1954,keratinisoform_k6e_(krt6e)_mrna,_complete_cds_
 m14676_1864-2332,src-like_kinase_(slk)_mrna,_complete_cds
 m95585mrna_3253-3805,hepatic_leukemia_factor_(hlf)_mrna,_complete_cds
 u41518_1761-2253,channel-like_integral_membrane_protein_(aqp-1)_mrna,_clone_aqp-1-

30 2344,_partial_cds
 u77180_55-511,macrophage_inflammatory_proteinbeta_(mip-3beta)_mrna,_complete_cds
 all_x06182_4474-5069,c-kit_proto-oncogene_mrna_
 x61123mrna_1212-1608,btg1_mrna_

35 Metagene 27
 ac002073cds#1_507-759:in_reversesequence,_23812-
 24010,_wugsc:dj515n1.2_gene_extracted_frompac_clone_
 hg3345-ht3522_at_hg3345-ht3522_pou_domain-containing_protein_

137036exon#2_29-92:in_reversesequence,_1754-1971,neutrophil-activating_peptide_78_(ena-
78)_gene,_com
m15169mma#1_1704-1950:in_reversesequence,_3390-3408,beta-2-
adrenergic_receptor_mrna,_complete_cds
5 m25756_1777-2287,secretogranin_ii_gene,_complete_cds
m28983_1823-2369,interleukinalpha_(il_1)_mrna,_complete_cds
m33317mma_1158-1693,cytochrome_p450iiia4_(cyp2a4)_mrna,_complete_cds
m62486exon_17-359:not_in_gb_record,c4b-binding_protein_gene_
u66580cds_510-1026:in_reversesequence,_1075-1081,putative_g_protein-
10 coupled_receptor_(gpr21)_gene,_c
u79242_1043-1589,clone_23560_mrna_sequence_
all_x02404_227-
750,mrna_fragment_for_second_calcitonin_gene_related_peptide_(cgrp)_from_medullary_th
x55005mrna_2002-2230,c-erba-1_mrna_for_thyroid_hormone_receptor_alpha_
15 x77533cds_982-1390:in_reversesequence,_1532-1544,mrna_for_activin_type_ii_receptor
all_z11933_1730-1942,mrna_for_n-oct_3,_n-oct5a,_and_n-oct_5b_proteins

Metagene 444

20 af014958_1175-1619,chemokine_receptor_x_(ckrx)_mrna,_complete_cds/gb=af014958_/ntype=rna
d16688_876-1448,ltg9/mlt3_mrna,_c-terminal
d29956_3758-4328,mrna_for_kiaa0055_gene,_complete_cds
d31888_4700-5186,mrna_for_kiaa0071_gene,_partial_cds
d38037_292-826,mrna_for_fk506-binding_protein_12kda_(hfkbp-12)_homologue,_complete_cds
25 d63135mma_31-499,mrna_for_ets-like_30_kda_protein/gb=d63135_/ntype=rna
d79987_6109-6523,mrna_for_kiaa0165_gene,_complete_cds
d86957_3869-4265,mrna_for_kiaa0202_gene,_partial_cds
d88213_2085-2481,mrna_for_retina-specific_amine_oxidase,_complete_cds
hg2383-ht4824_s_at_hg2383-ht4824_cystathionine_beta_synthase,_alts splice_3
30 hg25930-ht26386_at_hg25930-ht26386_estradiol_17-beta_dehydrogenase
hg2841-ht2968_s_at_hg2841-ht2968_albumin,_alts splice_1
hg2987-ht3136_s_at_hg2987-ht3136_vasoactive_intestinal_peptide_
hg3264-ht3441_at_hg3264-ht3441_af-6
hg4027-ht4297_f_at_hg4027-ht4297_beta-1-glycoprotein,_domains_n_and_iia,_pregnancy-specific
35 hg4390-ht4660_at_hg4390-ht4660_ribosomal_protein_l18a_homolog
l06133_7979-8435,putative_cu++-transporting_p-type_atpase_mrna,_complete_cds
all_108904_1372-1667,h2k_binding_factor(kbf2)_mrna,_complete_cds
112468_3246-3780,aminopeptidase_a_mrna,_complete_cds
114812_3349-3936,retinoblastoma_related_protein_(p107)_mrna,_complete_cds

120826_3074-3572,i-plastin_mrna,_complete_cds
 122569_1685-2243,cathepsin_b_mrna,_3'_utr_with_a_stem-loop_structure_providing_mrna_stability_
 139060mrna_1037-1547,transcription_factor_s11_mrna,_complete_cds
5 m11025mrna_783-1263,asialoglycoprotein_receptor_h2_mrna,_complete_cds
 m17252mrna_934-1198,cytochrome_p450c21_mrna,_3'_end
 all_m24364_1059-
 1435,mhc_ii_lymphocyte_antigen_dqb_mrna,_complete_cds,_haplotype_dr7,_dqw9_
 m29581_1469-1853,zinc-finger_protein(zfp8)_mrna,_3'_end_
10 m57464_3899-4439,ret_proto-oncogene_mrna,_complete_cds_
 m63962mrna_2985-3507,gastric_h,k-atpase_catalytic_subunit_gene,_complete_cds
 m74525_2002-2536,hhr6b_(yeast_radhomologue)_mrna,_complete_cds
 m87860cds_25-331:in_reversesequence,_176-212,s-lac_lectin_1-14-ii_(lgals2)_gene_
 m89955cds_635-1085:in_reversesequence,_1391-1439,5-HT1d-
15 type_serotonin_receptor_gene,_complete_cds
 s48983cds_36-282:in_reversesequence,_204-
 408,_saa4=serum_amyloid_a_[human,_genomic,_858_ntsegments]
 s59184_2487-2979,_ryk=related_to_receptor_tyrosine_kinase_[human,_hepatoma,_mrna,_3068_nt]
 s61953_516-798,_c-
20 erbB3=receptor_tyrosine_kinase_{alternatively_spliced}_[_human,_gastric_cancer_cell
 u16811_1491-2034,bak_mrna,_complete_cds
 all_u18914_2694-3199,19.8_kda_protein_mrna,_complete_cds_
 u28758_45-626,nmda_receptor_subtype_2b_subunit_(grin2b)_mrna,_partial_cds
 u40215_1479-2049,synapsin_iib_mrna,_complete_cds_
25 u40763_2251-2803,clk-associated_rs_cyclophilin_cars-cyp_mrna,_complete_cds_
 u43286_1633-2155,selenophosphate_synthetase(sps2)_mrna,_complete_cds
 u44848_7-187,nuclear_respiratory_factor(nrf1)_mrna,_3'_utr/gb=u44848/_ntype=rna_
 u48807_1652-2156,map_kinase_phosphatase_(mkp-2)_mrna,_complete_cds_
 u49974cds_444-
30 1017,mariner2_transposable_element,_complete_consensus_sequence/gb=u49974/_ntype=dna /
 u52518_399-825,grb2-related_adaptor_protein_(grap)_mrna,_complete_cds
 u71092cds_954-1158:in_reversesequence,_1611-1767,somatostatin_receptor-like_protein_(slc1)_gene,_com
 u79257_952-1432,clone_23932_mrna_sequence
35 u88666_3113-3653,serine_kinase_srpk2_mrna,_complete_cds
 all_u90552_3170-
 3242,butyrophilin_(btf5)_mrna,_complete_cds, butyrophilin_(btf5)_mrna,_complete_cds
 u90912_1074-1584,clone_23865_mrna_sequence_
 u94332_761-1331,osteoprotegerin_(opg)_mrna,_complete_cds.

all_x06268_1159-1337,mrna_for_pro-alpha(ii)_collagen_3'_end_c-termtriple_helical_and_c-terminal_non-

all_x13956_694-1163,12s_rna_induced_by_poly(ri),_poly(rc)_and_newcastle_disease_virus
x15954mrna_729-1240,mbp1_gene,_exon(and_joined_cds)

5 x16707cds_379-733:in_reversesequence,_869-923,fra-1_mrna

x17360mrna_4536-5034,hox_5.1_gene_for_hox_5.1_protein_
all_x63575_3903-4466,mrna_for_plasma_membrane_calcium_atpase_

all_x64838_5256-5833,mrna_for_restin_

x66171cds_341-623:in_reversesequence,_892-1108,cmrf35_mrna,_complete_cds

10 all_x77383_1094-1599,mrna_for_cathepsin-o

x78031_1113-1629,alpha-1,_3-fucosyltransferase_mrna

all_x95289_48-625,mrna_for_hcgix_protein_

y11651cds_750-960:in_reversesequence,_1250-1466,mrna_for_phosphate_cyclase

15 Metagene 369

d86966_4491-5031,mrna_for_kiaa0211_gene,_complete_cds

d87074_6650-7184,mrna_for_kiaa0237_gene,_complete_cds

hg1862-ht1897_at_hg1862-ht1897_calmodulin_type_i_

20 hg825-ht825_at_hg825-ht825_guanine_nucleotide-binding_protein,_alpha_12

108424_1124-1586,achaete_scute_homologous_protein_(ash1)_mrna,_complete_cds_

123116_3296-3644,galactocerebrosidase_(galc)_mrna,_complete_cds_

m34715mrna_1750-2206,pregnancy-specific_beta-1-glycoprotein_mrna_psg95,_complete_cds_

m57423_485-1016,phosphoribosylpyrophosphate_synthetase_subunit_iii_mrna,_3'_end.

25 m80359_2409-2835,protein_p78_mrna,_complete_cds

s69370_234-

761,_pax3b=transcription_factor_{alternatively_spliced}_[human,_adult_cerebellum,_mrna,_8

u25750_3002-3380,chromosome_17q21_mrna_clone_1046:1-1

u35139_1111-1507,necidin_related_protein_mrna,_complete_cds_

30 u39447_3452-3980,placenta_copper_monamine_oxidase_mrna,_complete_cds_

u42390_8359-8863,trio_mrna,_complete_cds

u82130_1151-1451,tumor_susceptibility_protein_(tsg101)_mrna,_complete_cds_

x53793cds_873-

1227,ade2h1_mrnaShowing_homologies_to_saicar_synthetase_and_air_carboxylase_of_the_pu

35 x54150mrna_978-1530,mrna_for_fc_receptor_

x63422cds_305-461:in_reversesequence,_688-916,mrna_for_delta-

subunit_of_mitochondrial_f1f0_atp-synth

all_x63546_7261-7856,mrna_for_tre_oncogene_(clone_210)_

all_z25535_4922-5463,mrna_for_nuclear_pore_complex_protein_hnup153_

Metagene 441

d16350_1280-1826,sa_mrna_for_sa_gene_product,_complete_cds_

5 d38073_2590-3022,mrna_for_hrlf_beta_subunit_(p102_protein),_complete_cds_

d63481_4350-4890,mrna_for_kiaa0147_gene,_partial_cds_

142373mrna_2651-3071,protein_phosphatase_2a_b56-alpha_mrna,_complete_cds

m29277_2335-

2901,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_juso_muc18_

10 m34458mrna_1900-2463,lamin_b_mrna,_complete_cds_

u33286_2642-3092,chromosome_segregation_gene_homolog_cas_mrna,_complete_cds

u37426_4269-4815,kinesin-like_spindle_protein_hksp_(hksp)_mrna,_complete_cds_

u53204_14286-14721,plectin_(plec1)_mrna,_complete_cds

u56816_1376-1838,kinase_myt1_(myt1)_mrna,_complete_cds.

15 u73843_1356-1860,epithelial-specific_transcription_factor_ese-1b_(ese-1)_mrna,_complete_cds

all_x74331_1801-2288,mrna_for_dna_primate_(subunit_p58)

all_x99459_1516-1799,mrna_for_sigma_3b_protein_

y00486mrna_252-

786,_adenine_phosphoribosyltransferase_(aprt)_gene_extracted_fromaprt_gene_for_adenin

20 all_z22555_2041-2516,encoding_cla-1_mrna_

z37986cds_409-631:in_reversesequence,_826-1000,mrna_for_phenylalkylamine_binding_protein

Metagene 407

25 d28539_4017-4549,mrna_for_metabotropic_glutamate_receptor_subtype_5b,_complete_cds_

d83195cds_448-802:in_reversesequence,_3957-

3963,dnase1_gene_for_deoxyribonuclease_i,_complete_cds_

m21665mrna_1535-1621,beta-myosin_heavy_chain_mrna,_3'_end

m32315_3202-3604,tumor_necrosis_factor_receptor_mrna,_complete_cds_

30 z70295exon#2-3_7-252;not_in_gb_record,gcap-ii_gene

Metagene 390

d88795_13-379,mrna_for_cadherin,_partial_cds/gb=d88795_/ntype=rna_

35 d88797_49-379,mrna_for_cadherin,_partial_cds/gb=d88797_/ntype=rna_

hg273-hg273_s_at_hg273-hg273_lymphocyte_antigen_hla-g3_

hg3454-hg3647_at_hg3454-hg3647_zinc_finger_protein_

hg644-hg644_at_hg644-hg644_histone_h1.1

l35251mrna_801-1281,extracellular_matrix_protein_(mfap3)_gene,_complete_cds

all_m11437_1562-
 2440,_kng_gene_(kininogen)_extracted_fromkininogen_gene,_kng_gene_(kininogen)_extrac
 u28727_7835-8357,pregnancy-associated_plasma_protein-
 a_preproform_(pappa)_mrna,_complete_cds_

5 u43279_3409-3955,nucleoporin_nup_36_mrna,_complete_cds/gb=u43279_/ntype=rna
 x05615cds_7824-8238:in_reversesequence,_8327-8423,mrna_for_thyroglobulin
 x51823cds_5-34,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_partial/gb=x51823_/ntype=rna
 x82279exon_54-169,fas,_apo-

10 1_gene_(promoter_and_exon_i)/gb=x82279_/ntype=dna_annot=exon_-

Metagene 254

d28118_1807-2263,mrna_for_db1,_complete_cds

15 d45370mrna_13-
 337,apm2_mrna_for_gs2374_(unknown_product_specific_to_adipose_tissue),_complete_cds
 hg2465-ht4871_at_hg2465-ht4871_dna-binding_protein_ap-2,_altslice_3_-
 m31682mrna_2130-2526,testicular_inhibin_beta-b-subunit_mrna,_3'_end
 m86933_220-

20 681,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds
 u28249_919-1405,11kd_protein_mrna,_complete_cds
 u68031_91-301,g_protein-
 coupled_receptor_(strl22)_mrna,_alternatively_spliced_5'_utr_sequence/gb=u68
 x76732cds_975-1221:in_reversesequence,_1464-

25 1518:not_in_gb_record,nefa_protein_mrna,_complete_cds_(d

Metagene 399

d87328_5900-6404,mrna_for_hcs,_complete_cds

30 j05096mrna_5006-5456,na,k-atpase_subunit_alpha(atp1a2)_gene,_complete_cds
 reverse_l76568_31050-
 31356,_s26_fromexcision_and_cross_link_repair_protein_(ercc4)_gene,_complete_ge
 all_u67092_1093-1868:not_in_gb_record,ataxia-
 telangiectasia_locus_protein_(atm)_gene,_exons_1a,_1b,_

35 all_x13227_1080-1567,mrna_for_d-amino_acid_oxidase_(ec_1.4.3.3)
 x59710cds_75-585:in_reversesequence,_714,mrna_for_caat-
 box_dna_binding_protein_subunit_b_(nf-yb)
 x64559cds_202-580:in_reversesequence,_679-823,mrna_for_tetranectin

Metagene 275

j04168_1867-2263,leukosialin_mrna,_complete_cds
 105515_2108-2594,camp_response_element-binding_protein_(cre-bp1)_mrna,_complete_cds_
 5 109190mrna_6480-6930,trichohyalin_(trhy)_gene,_complete_cds_
 m26602_181-469,defensinprotein_mrna,_complete_cds_
 u79245_1139-1541,clone_23586_mrna_sequence_
 u82668mrna#2_1298-
 1820,_shox_gene_(shoxb)_extracted_fromshox_gene,_alternatively_spliced_products,_c
 10 z18954exon#1-4_126-240:in_reversesequence,_246-264,mrna_for_s100d_calcium_binding_protein_

Metagene 268

d63483_2777-3304,mrna_for_kiaa0149_gene,_complete_cds
 15 104510_2769-3285,nucleotide_binding_protein_mrna,_complete_cds_
 m25322mrna_2577-3039,granule_membrane_protein-140_mrna,_complete_cds_
 s76978_29-224,_prostate-specific_membrane_antigen_{alternatively_spliced}_*[human,_primary_prostatic_
 u33429_2481-2994,k+_channel_betasubunit_mrna,_complete_cds

20

Metagene 250

d00760_277-781,mrna_for_proteasome_subunit_hc3_
 d14710_1298-1808,mrna_for_atp synthase_alpha_subunit,_complete_cds_
 25 d15057_162-576,mrna_for_dad-1,_complete_cds
 d78151_2321-2825,mrna_for_26s_proteasome_subunit_p97,_complete_cds_
 d78275_959-1511,mrna_for_proteasome_subunit_p42,_complete_cds
 hg1112-ht1112_at_hg1112-ht1112_ras-like_protein_tc4
 hg2855-ht2995_at_hg2855-ht2995_heat_shock_protein,_70_kda
 30 hg3214-ht3391_at_hg3214-ht3391_metallopanstimulin_
 j02683mrna_629-1066,adp/atp_carrier_protein_mrna,_complete_cds_
 j02902mrna_1694-2156,protein_phosphatase_2a_regulatory_subunit_alpha-isotype_(alpha-pr65)_mrna,_comp
 j04173_1114-1648,phosphoglycerate_mutase_(pgam-b)_mrna,_complete_cds
 35 j04973mrna_1023-1485,cytochrome_bc-1_complex_core_protein_ii_mrna,_complete_cds
 l03532_1898-2372,m4_protein_mrna,_complete_cds
 l07633_396-870,(clone_1950.2)_interferon-gamma_ief_ssp_5111_mrna,_complete_cds
 l26247_131-617,suili01_mrna,_complete_cds
 l41351mrna_1269-1695,prostasin_mrna,_complete_cds_

176159mrna_471-957,frg1_mrna,_complete_cds
 m17733mrna_13-505,thymosin_beta-4_mrna,_complete_cds_
 m38690_584-1106,cd9_antigen_mrna,_complete_cds_
 m55265mrna_1612-2116,casein_kinase_ii_alpha_subunit_mrna,_complete_cds_
5 m57730mrna_975-1437,b61_mrna,_complete_cds_
 m63488_1834-2344,replication_protein_a_70kda_subunit_mrna_complete_cds_
 m93651_1973-2519,set_gene,_complete_cds
 s80343_1609-2077,_args=arginyl-tRNA_synthetase_[human,_ataxia-telangiectasia_patients,_ebv-
 lymphobl
10 u03100_2985-3501,alpha2(e)-catenin_mrna,_complete_cds
 u06155cds_43-
 495,chromosome_1q_subtelomeric_sequence_d1s553/gb=u06155_ntype=dna_annot=cds,chromoso
 u15008_25-433,snrnp_core_protein_sm_d2_mrna,_complete_cds
 u18919_408-948,chromosome_17q12-21_mrna,_clone_pov-2,_partial_cds
15 u25849mrna_1717-2137,red_cell-
 type_low_molecular_weight_acid_phosphatase_(acp1)_gene,_5'_flanking_re
 u30825_528-1014,splicing_factor_srP30c_mrna,_complete_cds
 u32944_162-540,cytoplasmic_dynein_light_chain(hdcl1)_mrna,_complete_cds_
 u38846_1294-1732,stimulator_of_tar_rna_binding_(srB)_mrna,_complete_cds
20 u39317_16-484,e2_ubiquitin_conjugating_enzyme_ubch5b_(ubch5b)_mrna,_complete_cds_
 u51678_276-756,small_acidic_protein_mrna,_complete_cds_
 u52427mrna_239-773,rna_polymerase_ii_seventh_subunit_(rpB-7)_gene,_complete_cds.
 u60276_645-1191,hasna-i_mrna,_complete_cds_
 u73514_376-892,short-chain_alcohol_dehydrogenase_(xh98g2)_mrna,_complete_cds.
25 u73824_3202-3766,p97_mrna,_complete_cds
 u77396_at_u77396_u77396,not_in_gb_record,tnf-
 alpha_inducible_responsive_element_mrna,_complete_cds
 x00351cds_855-1065:in_reversesequence,_1154-1376,mrna_for_beta-actin
 all_x15183_2479-2894,mrna_for_90-kda_heat-shock_protein
30 all_x53331_31-590,mrna_for_matrix_gla_protein
 all_x57206_3916-4487,mrna_for_1d-myo-inositol-trisphosphate_3-kinase_b_isoenzyme_
 x57959cds_264-714,mrna_for_ribosomal_protein_17
 x60036cds_683-1037:in_reversesequence,_1163-
 1223,mrna_for_mitochondrial_phosphate_carrier_protein_
35 x63563cds_3176-3500,mrna_for_rna_polymerase_ii_140_kda_subunit_
 x75091cds_300-653:in_reversesequence,_848-892,mrna_for_hla-dr_associated_protein_ii_(phapii)
 all_x81817_933-1240,bap31_mrna_
 x83218cds_215-539,mrna_for_atp_synthase
 all_x96752_1367-1818,mrna_for_l-3-hydroxyacyl-coa_dehydrogenase

y12711_336-864,mrna_for_putative_progesterone_binding_protein
z35402mrna_3912-4402,gene_encoding_e-cadherin,_exonand_joined_cds
z50853cds_556-802:in_reversesequence,_833-1001,mrna_for_clpp

5 Metagene 67

hg2171-ht2241_at_hg2171-ht2241_12-lipoxygenase_
m97347_1499-2060,beta-1,6-n-acetylglucosaminyltransferase_mrna,_complete_cds_
u46116mrna_5907-6477,receptor_tyrosine_phosphatase_gamma_(ptprg)_gene
10 all_u83600_202-
527,death_domain_receptor(ddr3)_mrna,_alternatively_spliced_form_2,_partial_cds/gb=u8
all_x95715_1306-1901,mrna_for_anthracycline_resistance_associated_protein

Metagene 293

15 102320_1463-1997,radixin_mrna,_complete_cds
m86868_1189-1585,gamma_amino_butyric_acid_(gaba_rho2)_gene_mrna,_complete_cds

Metagene 448

20 ab000449_1091-1607,mrna_for_vrk1,_complete_cds_
d14689_6077-6557,mrna_for_kiaa0023_gene,_complete_cds
x55668mrna_550-940,mrna_for_proteinase_3_
all_x75917_1064-1602,mrna_for_fetal_beta-mhc_binding_factor

25 Metagene 127

l24470_1905-2403,prostanoid_fp_receptor_mrna,_complete_cds
all_m36089_2244-2797,dna-repair_protein_(xrcc1)_mrna,_complete_cds
30 m74161_2469-2991,inositol_polyphosphate_5-phosphatase_(5ptase)_mrna,_3'_end
s57235_1085-
1664,_cd68=110kda_transmembrane_glycoprotein_[human_promonocyte_cell_line_u937,_mrna,_1
u48231exon#2_1478-2015,bradykinin_b1_receptor_(bdkrb1)_gene,_first_
x51630mrna_2403-2955:in_reversesequence,_2961-
35 2979,wilms_tumor_wt1_mrna_for_zinc_finger_protein,_kru
x98261cds_121-352:in_reversesequence,_388-583,mrna_for_m-phase_phosphoprotein,_mpp5_-

Metagene 134

hg4128-ht4398_at_hg4128-ht4398_anion_exchanger_3_cardiac_isoform
 j03934_1835-2371,_human,_nad(p)h:menadione_oxidoreductase_mrna,_complete_cds
 l00634_734-1246,farnesyl-protein_transferase_alpha-subunit_mrna,_complete_cds
 l09717mrna_1316-1778,lysosomal_membrane_glycoprotein-
5
 2_(lamp2)_gene,_5'_end_and_flanking_region
 110413_1331-1589,farnesyltransferase_alpha-subunit_mrna,_complete_cds
 120852_2574-3150,leukemia_virus_receptor(glvr2)_mrna,_complete_cds
 l37199_977-1313,(clone_cd24-1)_huntington_disease_candidate_region_mrna_fragment
 l42025mrna_1988-2504,cellular_co-factor_(rab)_gene,_complete_cds_
10
 m23114mrna_3623-4085,calcium-atpase_(hk1)_mrna,_complete_cds
 m55150mrna_978-1422,fumarylacetate_hydrolase_mrna,_complete_cds_
 m91592_1971-2325,zinc-finger_protein_(znf76)_gene,_partial_cds_
 s82447_42-397,_gcn5-
 like_1=gcn5_homolog/putative_regulator_of_transcriptional_activation_{clone_gcn5
15
 u10324_2934-3444,nuclear_factor_nf90_mrna,_complete_cds
 u24169_723-1197,jtv-1_(jtv-1)_mrna,_complete_cds_
 u24183_2457-3031,phosphofructokinase_(pfkm)_mrna,_complete_cds_
 u29091_960-1368,selenium-binding_protein_(hsbp)_mrna,_complete_cds/gb=u29091/_ntype=rna
 u29463mrna_2121-2681,cytochrome_b561_gene
20
 u40462_3034-3574,ikaros/lyf-1_homolog_(hik-1)_mrna,_complete_cds_
 u52153_2069-2513,inwardly_rectifying_potassium_channel_kir3.2_mrna,_complete_cds_
 u65676_3144-3648,hermansky-pudlak_syndrome_protein_(hps)_mrna,_complete_cds
 u66669_785-1240:not_in_gb_record,3-hydroxyisobutyryl-
 coenzyme_a_hydrolase_mrna,_complete_cds
25
 u68063_1453-1915,transformer-2_beta_(htra-2_beta)_mrna,_complete_cds_
 u74612_2915-3425,hepatocyte_nuclear_factor-3/fork_head_homolog_11a_(hfh-
 11a)_mrna_complete_cds.
 u75370_3396-
 3732,mitochondrial_rna_polymerase_mrna,_nuclear_gene_encoding_mitochondrial_protein,_com
30
 u76272mrna_161-689,diadenosine_triphosphate_(ap3a)_hydrolase_(fhit)_gene,_5'_of
 u91316_891-1461,acyl-coa_thioester_hydrolase_mrna,_complete_cds
 all_x06825_679-1154,mrna_for_skeletal_beta-tropomyosin_
 x15187cds_2089-2380:in_reversesequence,_2521-
 2737,tra1_mrna_forhomologue_of_murine_tumor_rejection_a
35
 x61970cds_299-677:in_reversesequence,_758-860,mrna_for_macropain_subunit_zeta_
 all_x70944_2459-3030,mrna_for_ptb-associated_splicing_factor_
 all_x77922_1492-2000,gd3_synthase_mrna_
 x85134mrna_2737-3007,rbq-3_mrna_
 all_x87176_2148-2593,mrna_for_17-beta-hydroxysteroid_dehydrogenase_

all_x91788_857-1284,mrna_for_icln_protein
 x95586exon#3_56-248:in_reversesequence,_5872-6088:not_in_gb_record,mb1_gene
 x97795cds_1954-2218:in_reversesequence,_2342-2564,mrna_homologous_to_scerevisiae_rad54
 y08682mrna_2358-2552,mrna_for_carnitine_palmitoyltransferase_i_type_i
5 y11251_4297-4822,mrna_for_novel_member_of_serine-arginine_domain_protein_srrp129
 z17227_1268-1850,mrna_for_transmenbrane_receptor_protein
 z68129mrna#1_3-469:in_fullsequence,_16183-16321:not_in_gb_record,h-
 idh_gamma_gene_(nad(h)-specific_

10 Metagene 466

hg3920-ht4521_s_at_hg3920-ht4521_homeotic_protein_a1,_i,_altslice_1_
 hg4517-ht4920_s_at_hg4517-
 ht4920_immunoglobulin_recombination_signal_sequence_binding_protein_altspl

15 l34155_4838-5306,laminin-related_protein_lama3_mrna,_complete_cds
 m21305cds_39-
 119,alpha_satellite_and_satellitejunction_dna_sequence/gb=m21305_ntype=dna_annot=cds
 u60808_1423-2000,cdp-diacylglycerol_synthase_(cds)_mrna,_complete_cds
 x60673mrna_1091-1649,ak3_mrna_for_adenylate_kinase_3

20
 Metagene 100

d28423_53-100,mrna_for_pre-
 mrna_splicing_factor_srps20,_5'_utr_(sequence_from_the_5'_cap_to_the_start

25 all_d89377_1587-2173,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
 l113943_1963-2019,glycerol_kinase_gk_mrna_exons_1-4,_complete_cds
 m37197mrna_2687-3065,ccaat-box-binding_factor_cbf_mrna,_complete_cds
 m68520_1708-2170,cdc2-related_protein_kinase_mrna,_complete_cds
 s67970_962-1538,_znf75=krab_zinc_finger_[human,_lung_fibroblast,_mrna,_1563_nt]_

30 s70585mrna_138-612,_thyroid-
 stimulating_hormone_alpha_subunit_[human,_genomic,_1327_ntsegments]_
 s82471_77-298,_ssx3=kruppel-
 associated_boxContaining_ssx_gene_[human,_testis,_mrna_partial,_675_nt]

35 u04209_1396-1834,associated_microfibrillar_protein_mrna,_complete_cds
 u12978_1713-2247,sperm_membrane_protein_bs-84_(hsd-1)_mrna,_partial_cds
 u15555_1003-1489,serine_palmitoyltransferase_lcb2_mrna,_partial_cds
 u18271_cds1_at_u18271_u18271,not_in_gb_record,thymopoietin_tpmo_gene,thymopoietin_tpmo
 _gene
 u39226_6864-7440,myosin_viiia_ush1b_mrna,_complete_cds

u43843_813-1374,h-neuro-d4_protein_mrna,_complete_cds
 u82321_1608-2112,clone_14.9b_mrna_sequence_
 all_x59618_1970-2475,rr2_mrna_for_small_subunit_ribonucleotide_reductase_
 x98482mrna_2-
5 46,tnt2_gene_exon/gb=x98482_/ntype=dna/_annot=mrna,tnt2_gene_exon/gb=x98482_/ntype=dn

Metagene 59

af001548mrna_6079-
10 6385,_815a9.1_gene_(myosin_heavy_chain)_extracted_fromchromosomebac_clone_cit987sk
 d15049_3317-3845,mrna_for_protein_tyrosine_phosphatase_
 l36531mrna_2573-3059,integrin_alpha5subunit_mrna,_3'_end
 l41680_1371-1869,alpha-2,8-polysialyltransferase_(pst)_gene,_complete_cds_
 m17316exon_3-249:in_reversesequence,_260-338:not_in_gb_record,gamma-a-
15 crystallin_gene_(gamma-g5)_
 m26061mrna_2449-2890:not_in_gb_record,cgmp_phosphodiesterase_alpha_subunit_(cgpr-
 a)_mrna,_complete_c
 m73482mrna_757-1279,neuromedin_b_receptor_(nmb-r)_mrna,_complete_cds_
 u43916_147-698,tumor-associated_membrane_protein_homolog_(tmp)_mrna,_complete_cds
20 u46744_2358-2493,dystrobrevin-alpha_mrna,_complete_cds_
 u94747_838-1276,wd_repeat_protein_han11_mrna,_complete_cds/gb=u94747_/ntype=rna
 all_x74142_1952-2535,hbf-1_mrna_for_transcription_factor_
 y09445cds_1175-1517:in_reversesequence,_2206-2368,mrna_for_transcription_factor_tbx5_

25 Metagene 87

j05070_1805-2303,type_iv_collagenase_mrna,_complete_cds
 u22028utr#1_47-
 168:in_reversesequence,_8031,cytochrome_p450_(cyp2a13)_gene,_complete_cds,cytochrome_
30 u77968_1294-1879,neuronal_pas1_(npas1)_mrna,_complete_cds
 x87767exon_4-148,cd89_gene,_exon_s1/gb=x87767_/ntype=dna/_annot=exon_

Metagene 195

35 d87461_2959-3517,mrna_for_kiaa0271_gene,_complete_cds
 m26004_3326-3894,cr2/cd21/c3d/epstein-barr_virus_receptor_mrna,_complete_cds_
 m65254_1710-2184,_protein_phosphatase_2a_65_kda_regulatory_subunit-beta_mrna,_complete_cds
 s81243_2102-
 2660,_chn=steroid/thyroid_orphan_receptor_homolog_gene_[human,_fetal_brain,_mrna_partial

u04847_1262-1802,inil_mrna,_complete_cds_
 u18383mrna_2319-2587,nuclear_respiratory_factor(nrf-1)_gene_
 u19147_34-66,gage-6_protein_mrna,_complete_cds_
 u51920_1447-1927,signal_recognition_particle_(srp54)_mrna,_complete_cds
5 u79290_1380-1770,clone_23908_mrna_sequence_
 u97502mrna_2736-3126,butyrophilin_(bt3.3)_gene_
 all_x51757_1909-2414,heat-shock_protein_hsp70b'_gene_
 x95152mrna_10974-11274,brca2_gene_exon(and_joined_coding_region)_
 y10812_767-1253,mrna_for_fructose-bisphosphatase_

10
 Metagene 489

m92287_1531-1999,cyclin_d3_(ccnd3)_mrna,_complete_cds_
 u32989_1109-1559,tryptophan_oxygenase_(tdo)_mrna,_complete_cds_

15 u90907_1150-1612,clone_23907_mrna_sequence_
 all_x99268_928-1367,mrna_for_b-hlh_dna_binding_protein_

Metagene 451

20 d10923_1452-1962,mrna_for_hm74_
 d42038_3730-4216,mrna_for_kiaa0087_gene,_complete_cds
 d50917_4943-5489,mrna_for_kiaa0127_gene,_complete_cds
 d50918_4053-4563,mrna_for_kiaa0128_gene,_partial_cds_
 hg2530-ht2626_at_hg2530-ht2626_adenylyl_cyclase-associated_protein

25 hg2796-ht2904_at_hg2796-ht2904_neural_cell_adhesion_molecule_
 hg3248-ht3425_at_hg3248-ht3425_fibroblast_growth_factor,_antisense_mrna
 all_k01884_587-888,blym-1_transforming_gene,_complete_coding_region
 105568_1937-2459,na+/cl_-dependent_serotonin_transporter_mrna,_complete_cds
 110374_1461-1977,(clone_ctg-a4)_mrna_sequence

30 111695_1767-2247,activin_receptor-like_kinase_(alk-5)_mrna,_complete_cds_
 113436mrna_3522-4020,guanylate_cyclase_mrna,_complete_mature_peptide
 120321_3112-3655,protein_serine/threonine_kinase_stk2_mrna,_complete_cds_
 122206exon#3_63-639,vasopressin_receptor_v2_gene,_complete_cds_
 138500cds_1574-2102,na+/myo-

35 inositol_cotransporter_(slc5a3)_gene,_complete_cds/gb=l38500_ntype=dna_
 l77563mrna_129-591,dgs-f_partial_mrna/gb=l77563_ntype=rna
 reverse_178833_2267-
 2337,_brcal_gene_extracted_frombrcal,_rho7_and_vati_genes,_complete_cds,_and_ipf
 m17863mrna_242-822,preproinsulin-like_growth_factor_ii_(igf-ii)_variant_mrna,_complete_cds_

all_m19720_2034-2557,_l-myc_gene_(l-myc_protein)_extracted_from_l-myc_protein_gene,_complete_cds,_l-m
 m25164cds_5-383:in_reversesequence,_265-1170,thyrotropin_beta_subunit_gene
 m55268mrna_1094-1556,casein_kinase_ii_alpha'_subunit_mrna,_complete_cds
5 m62302_1939-2485,growth/differentiation_factor(gdf-1)_mrna,_complete_cds
 m64788_2759-3209,gtpase_activating_protein_(rap1gap)_mrna,_complete_cds
 m65290_1957-2215,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds,_clone_p40_
 m95549_1774-2194,sodium/glucose_cotransporter-like_protein_mrna,_complete_cds_
 m98776mrna_1864-2266,keratin_gene,_complete_cds_
10 s78432mrna#1_3-87,_un-named-transcript-
 1_from_sas=transmembraneprotein_{5'_region}_[human,_sarcomas,
 u10686exon#2_730-1267,mage-11_antigen_(mage11)_gene,_complete_cds
 u12897_1564-1870:in_reversesequence,_1900-1996,non-translated_mrna_sequence_
 u15173_1781-2303,nip2_(nip2)_mrna,_complete_cds
15 u23736_779-1348,gata-3_binding_protein_g3b_mrna,_partial_cds.
 u28831_532-964,protein_immuno-reactive_with_anti-pth_polyclonal_antibodies_mrna,_partial_cds_
 u37352_3505-3961,protein_phosphatase_2a_b'alpha1_regulatory_subunit_mrna,_complete_cds_
 u37431mrna#1_2114-
 2540,hoxa1_mrna,_long_transcript_and_alternatively_spliced_forms,_complete_cds_
20 u43527_180-728:not_in_gb_record,malignant_melanoma_metastasis-suppressor_(kiss-1)_gene,_mrna,_comple
 u43944_1705-1978,breast_cancer_cytosolic_nadp(+)-dependent_malic_enzyme_mrna,_partial_cds
 u47931mrna_63-537,g-protein_beta-
 3_subunit_alternatively_spliced_form_mrna_sequence/gb=u47931_/ntype
25 u52830_19-271,cri-du-chat_region_mrna,_clone_csc8.
 u55209_3812-3977,myosin_vii_a_transcriptmrna,_complete_cds_
 u63329cds_1128-1554:in_reversesequence,_1814,muty_homolog_(hmyh)_gene,_complete_cds_
 u84011_6566-
 7127,glycogen_debranching_enzyme_isoform(agl)_mrna,_alternatively_spliced_isoform,_compl
30 x04145cds_286-454:in_reversesequence,_593-689,mrna_for_t-cell_receptor_t3_gamma_polypeptide_
 x14690cds_1150-1604:in_reversesequence,_1636-1676,mrna_for_plasma_inter-alpha-trypsin_inhibitor_heav
 all_x16983_3252-3787,mrna_for_integrin_alpha-4_subunit_
35 all_x65962_1115-1174,mrna_for_cytochrome_p-450_
 all_x79984_16-269,aa1_mrna/gb=x79984_/ntype=rna
 x89398exon#7_695-1121,_ung_gene_(uracil-dna-glycosylase,_ung2)_extracted_from_ung_gene_for_uracil_dna
 all_z48541_4517-5100,mrna_for_protein_tyrosine_phosphatase_

z48579cds_1852-2050:in_reversesequence,_2062-2392,mrna_for_disintegrin-
 metalloprotease_(partial)_
 reverse_z84722_11257-
 11453,dna_sequence_from_cosmid_gg4_from_a_contig_from_the_tip_of_the_short_arm_

5

Metagene 252

d10326_1427-1981,mrna_for_pyruvate_kinase
 d49372_197-755,mrna_for_eotaxin,_complete_cds
 10 all_d83407_2601-3184,_zaki-4_mrna_inskin_fibroblast,_complete_cds
 d87467_5371-5857,mrna_for_kiaa0277_gene,_complete_cds
 hg167-ht167_s_at_hg167-ht167_hypothetical_protein_npiiy20
 hg2810-ht2921_at_hg2810-ht2921_homeotic_protein_pl2
 hg3162-ht3339_at_hg3162-ht3339_transcription_factor_iia
 15 hg3627-ht3836_at_hg3627-ht3836_calcium_channel,_voltage-
 gated,_betasubunit,_1_type,_altssplice_2,_ske
 hg3638-ht3993_s_at_hg3638-ht3993_amyloid_beta_(a4)_precursor_protein,_alts splice_4
 hg4169-ht4439_s_at_hg4169-ht4439_syntaxin_1b_
 hg830-ht830_at_hg830-ht830_potassium_channel_
 20 j02645mrna_882-1314,translational_initiation_factor_(eif-2),_alpha_subunit_mrna,_complete_cds
 k02777_139-621,t-cell_receptor_active_alpha-chain_mrna_from_jurkat_cell_line_
 100354exon_7-361:not_in_gb_record,cholecystokinin_(cck)_gene
 143821mrna_3222-3774,enhancer_of_filamentation_(hef1)_mrna,_complete_cds
 all_m15517_182-
 25 480,_ttr_gene_extracted_frommutant_prealbumin_gene_directly_linked_to_familial_amyloi
 all_m17183_531-752,parathyroid_hormone-related_protein_mrna,_complete_cds
 all_m17466_3487-4040,blood_coagulation_factor_xii_(f12)_gene_
 m20642mrna_369-898,alkali_myosin_light_chainmrna,_complete_cds
 m69238_2033-2579,aryl_hydrocarbon_receptor_nuclear_translocator_(arnt)_mrna,_complete_cds
 30 m90299mrna_2142-2628,glucokinase_(gck)_mrna,_complete_cds
 s43646_1904-2402,_cytokeratin[human,_epidermis,_mrna,_2427_nt]_
 s77582_2-
 55,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt240}_[human,_multiple_sclerosis,_
 s78798_1252-1687,_1-phosphatidylinositol-4-phosphate_5-
 35 kinase_isoform_c_[human,_peripheral_blood_leu
 s79219_344-902,_metastasis-
 associated_gene_[human,_highly_metastatic_lung_cell_subline_anip[937],_mr
 s82592_357-861,_evi-1=evi-
 1_protein_{3'_region_deletion_region}_[human,_megakaryoblastoid_cell_line

u13219_1945-2473,forkhead_protein_freac-1_mrna,_complete_cds_
 u18549exon#2_1091-1571,gpr6_g_protein-coupled_receptor_gene,_complete_cds
 u40317_5400-5965,protein_tyrosine_phosphatase_ptpsigma_(ptpsigma)_mrna,_complete_cds_
 u49250_2323-2851,putative_cerebral_cortex_transcriptional_regulator_t-brain-1_(tbr-
5
 1)_mrna,_complete
 u58130_2887-3301,bumetanide-sensitive_na-k-2cl_cotransporter_(nkcc2)_mrna,_complete_cds
 u67615_12883-13381,beige_protein_homolog_(chs)_mrna,_complete_cds
 u77846mrna_979-
 1356,elastin_gene,_partial_cds_and_partial_3'_utr,elastin_gene,_partial_cds_and_parti
10
 u79277_986-1520,clone_23548_mrna_sequence
 u89995_3040-3460,dna_binding_protein_fkhl15_(fkhl15)_mrna,_complete_cds
 u92015_605-1031,clone_143789_defective_mariner_transposon_hsmar2_mrna_sequence_
 all_x07876_1706-2205,mrna_for_irp_protein_(int-1_related_protein)
 x16706cds_541-931:in_reversesequence,_970,fra-2_mrna
15
 x54380mrna_4050-4590,mrna_for_pregnancy_zone_protein
 all_x64269_2501-2754,gene_mtfl_for_mitochondrial_transcription_factor_1_
 x68561cds_2234-2324:in_reversesequence,_2547-2943,spr-1_mrna_for_gt_box_binding_protein_
 all_x69920_2736-3249,mrna_for_calcitonin_receptor
 all_x73079_2348-2919,encoding_polymeric_immunoglobulin_receptor_
20
 all_x77737_992-1431,mrna_for_red_cell_anion_exchanger_(epb3,_ae1,_band_3)_3'_non-
 coding_region
 all_x78342_1655-1857,pisslre_mrna
 x78711cds_1553-1638:in_reversesequence,_1665-1735,mrna_for_glycerol_kinase_testis_specific_1
 x87871cds_939-1367:in_reversesequence,_1472-1588,mrna_for_hepatocyte_nuclear_factor_4b
25
 all_x90846_2935-3407,mrna_for_mixed_lineage_kinase_2,mrna_for_mixed_lineage_kinase_2
 x91220_3940-4165,mrna_for_na-cl_electroneutral_thiazide-sensitive_cotransporter
 all_z11502_886-1451,mrna_for_intestine-specific_annexin
 z48051mrna_1733-2303,gene_for_myelin_oligodendrocyte_glycoprotein_(mog)_
 all_z70218_2-333,mrna_for_nn1_protein_(clone_icrfp507i0498)
30
 all_z73903_5001-5554,mrna_for_trpc1a.
 z96810cds_482-968,dna_sequence_from_pac_452h17_on_chromosome_x_contains_sodium-
 and_chloride-dependen

Metagene 334

35

d13146mrna#1_2083-2551,_2',3'_cyclic-nucleotide_3'_-
 phosphodiesterase_gene_extracted_from2',3'_-c
 d21235_1418-1673,mrna_for_hhr23a_protein,_complete_cds_
 d83702_2392-2902,brain_mrna_for_photolyase_homolog,_complete_cds_

d87452_3950-4418,mrna_for_kiaa0263_gene,_complete_cds
d87459_2144-2564,mrna_for_kiaa0269_gene,_complete_cds
113848_3675-4161,rna_helicase_a_mrna,_complete_cds_
120591exon_1-295:not_in_gb_record,annexin_iii_(anx3)_gene,_alternative
5 m22348_3-494,mitochondrial_ubiquinone-binding_protein_mrna,_complete_cds_
s74017_1721-2213,_nrf2=nf-e2-
like_basic_leucine_zipper_transcriptional_activator_[human,_hemin-induc
s75313_1197-1387,_mjd1=mjd1_protein_{cag_repeats}_[human,_brain,_mrna,_1776_nt]_
u19765exon#5_630-1194,nucleic_acid_binding_protein_gene,_complete_cds
10 u64105_2540-3104,guanine_nucleotide_exchange_factor_p115-rhogef_mrna,_partial_cds
u67156_4641-5151,mitogen-activated_kinase_kinase_kinase(mapkkk5)_mrna,_complete_cds_
all_x06318_2381-2541,mrna_for_protein_kinase_c_(pkc)_type_beta_i_
x55740mrna_2940-3516,placental_cdna_coding_for_5'_nucleotidase_(ec_3.1.3.5)
all_x76648_338-777,mrna_for_glutaredoxin_
15 z78291_28-223,mrna_(clone_1d8).

Metagene 311

d13305_1572-1992,mrna_for_brain_cholecystokinin_receptor_
20 d55640_110-635,monocyte_pabl_(pseudoautosomal_boundary-
like_sequence)_mrna,_clone_mo2/gb=d55640_/nty
l19063exon_79-451,glial-
derived_neurotrophic_factor_gene,_complete_cds/gb=l19063_/ntype=dna/_annot=e
l39211_1877-2399,mitochondrial_carnitine_palmitoyltransferase_i_mrna,_complete_cds
25 m10051_4111-4651,insulin_receptor_mrna,_complete_cds_
m69203cds_4-254:in_reversesequence,_122-144,cytokine_(scya2)_gene_
u03644_1050-1452,recepin_mrna,_complete_cds
u17566_2214-2754,65_kda_hydrophobic_protein_mrna,_complete_cds_
u78628_7-
30 199_leukemia_inhibitory_factor_receptor_mrna,_5'_untranslated_region/gb=u78628_/ntype=rna_
x66363cds_1279-1459:in_reversesequence,_1594-1702,mrna_pctaire-
1_for_serine/threonine_protein_kinase
x85785mrna_1060-1498,darc_gene
x99076mrna_736-1234,nrgn_gene,_exons_2,3_&(joined_cds)_
35 y00451cds_1461-1890:in_reversesequence,_2009-2037,mrna_for_5-aminolevulinate_synthase_

Metagene 175

m31661_2134-2674,prolactin_(prl)_receptor_mrna,_complete_cds_

u12139exon_13-

151, alpha1(xi)_collagen_(col11a1)_gene,_5'_region_and_exon/gb=u12139_/ntype=dna/_annot

Metagene 43

5

d11086_976-1408,mrna_for_interleukinreceptor_gamma_chain

hg2090-ht2152_s_at_hg2090-ht2152_external_membrane_protein,_130_kda

hg2639-ht2735_s_at_hg2639-ht2735_single-stranded_dna-binding_protein_mssp-1

m30257_2214-2709,vascular_cell_adhesion_moleculemrna,_complete_cds

10

m33600_581-1109,mhc_ii_hla-dr-beta-1_(hla-drb1)_mrna,_complete_cds_

m37033_915-1395,cd53_glycoprotein_mrna,_complete_cds_

m60830exon_1480-2020,evi2b3p_gene,_exon_and_complete_cds_

m83221_1788-2262,i-rel_mrna,_complete_cds_

s73813_1337-

15

1775,_cd39=lymphoid_cell_activation_antigen_[human,_b_lymphoblastoid_cell_line,_mp-1,_mr

u95626mrna#3_2792-

3278,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_and_

x04500exon#7_244-778,gene_for_prointerleukinbeta

x56841mrna_1269-1713,hla-e_gene

20

all_x57522_2229-2788,ring4_cDNA

x64072cds_1948-2281:not_in_gb_record,_hsapiens_cd18_exon_2_

all_x99687_221-732,mrna_for_methyl-cpg-binding_protein_2,_intron/gb=x99687_/ntype=rna_

all_y00062_3996-4597,mrna_for_t200_leukocyte_common_antigen_(cd45,_lc-a)_

y09561cds_1238-1676:in_reversesequence,_1798,mrna_for_p2x7_receptor_

25

z14982mrna#1_616-1150,_mhc-encoded_proteasome_subunit_gene_lamp7-

e1_gene_(proteasome_subunit_lmp7)_e

Metagene 458

30

hg2339-ht2435_at_hg2339-ht2435_nuclear_factor_1,_variant_hepatic_

111702_2837-3335,phospholipase_d_mrna,_complete_cds

l38820exon_170-620,hmc_i_antigen-like_glycoprotein_(cd1d)_gene

m93119_2345-2777,zinc-finger_dna-binding_motifs_(ia-1)_mrna,_complete_cds

all_u34301_1497-

35

1528,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301_/ntyp

u66497_3549-4047,leptin_receptor_splice_variant_form_13.2_mrna,_complete_cds.

u73191_1078-1582,inward_rectifier_potassium_channel_(kir1.3),_complete_cds_

all_x75756_3248-3699,mrna_for_protein_kinase_c_mu

Metagene 222

d87444_3517-3823,mrna_for_kiaa0255_gene,_complete_cds
d89859_2331-2841,mrna_for_zinc_fingerprotein,_complete_cds
5 hg162-ht3165_at_hg162-ht3165_tyrosine_kinase,_receptor_axl,_altslice_2
hg33-ht33_at_hg33-ht33_ribosomal_protein_s4,_x-linked
106147_1586-2042,(clone_sy11)_golgin-95_mrna,_complete_cds_
110910_2084-2552,splicing_factor_(cc1.3)_mrna,_complete_cds_
m18737mrna_269-
10 815,_gja1p1_gene_extracted_fromhanukah_factor_serine_protease_(huhf)_mrna,_complete_c
all_m29277_2842-
2926,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_juso_mu
m33493_504-792,tryptase-iii_mrna,_3'_end_
m83822_6791-7253,beige-like_protein_(bgl)_mrna,_partial_cds
15 s52969_cds1_s_at_s52969_s52969,not_in_gb_record,_description:_alpha-
1,3_fucosyltransferase_gene_extr
u07620_1861-2215,map_kinase_mrna,_complete_cds_
u48705mrna_3326-3867,receptor_tyrosine_kinase_ddr_gene,_complete_cds
u63295_1285-1795,seven_in_absentia_homolog_mrna,_complete_cds
20 u67122_469-728,ubiquitin-related_protein_sumo-1_mrna,_complete_cds.
u70660_31-463,copper_transport_protein_hah1_(hah1)_mrna,_complete_cds
x80907_2095-2557,mrna_for_p85_beta_subunit_of_phosphatidyl-inositol-3-kinase_
x84707mrna_73-511,mia_gene
x89211cds_1571-
25 2129,dna_for_endogenous_retroviral_like_element/gb=x89211_/ntype=dna/_annot=cds_
all_z21966_1647-2182,mpou_homeobox_protein_mrna
z36715cds_1026-1200:in_reversesequence,_1491-1557,mrna_for_net_transcription_factor_

Metagene 249

30 m15780cds_13-
304,dna/endogenouspapillomavirus_type(hpv)_dna,_right_flank_and_viral_host_junction/gb=
m22092exon_6-42,neural_cell_adhesion_molecule_(n-
cam)_gene,_exon_sec_and_partial_cds/gb=m22092_/ntyp
35 u18004_31-205,_hsu18004cdna_

Metagene 432

ac002115_66940-67151:in_ac002115cds#2_675-
 1000,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping
 hg371-ht26388_s_at_hg371-ht26388_mucin_1,_epithelial,_altslice_9
 j05252_1611-2178,kex2-like_endoprotease_mrna,_complete_cds.
5 j05556mrna_1640-2198,collagenase_mrna,_complete_cds_
 all_m18255_18-408:in_m18255cds_47,_prkacb_gene_(protein_kinase_c-beta-
 2)_extracted_fromprotein_kinas
 m60614_1996-2060,wilms_tumor_(wit-1)_associated_protein_mrna,_complete_cds_
 s75213_1727-2087,_type-iva_cyclic_amp_specific_phosphodiesterase_hpde4a_[human,_t-
10 cells,_mrna_partia
 u00954_738-1224,clone_ce29_7.2_(cac)n/(gtg)n_repeat-containing_mrna
 u38904_1210-1744,zinc_finger_protein_c2h2-25_mrna,_complete_cds
 u45976_1748-
 2210,clathrin_assembly_protein_lymphoid_myeloid_leukemia_(calm)_mrna,_complete_cds_
15 u52682_4755-
 5241,lymphocyte_specific_interferon_regulatory_factor/interferon_regulatory_factor(lisrf
 u58096_798-1056,testis-specific_protein_(tspy)_mrna,_complete_cds
 u65406mrna#1_1860-2370,_kcnj1_gene_(potassium_channel_ron-
 k3)_extracted_fromalternatively_spliced_po
20 u71203_339-753,rit_mrna,_complete_cds
 u89336exon#13_173-
 695,_unknown_gene_extracted_fromhla_iii_regionContaining_notch4_gene,_partial_seq
 all_x16660_1795-2049,_open_reading_frame_p25_(aa_1-223)_gene_extracted_fromhtlv-
 i_related_endogenous
25 x71877cds_587-767:in_reversesequence,_783-1089,mrna_for_chymotrypsin-like_protease_ctrl-1
 all_x89894_2017-2486,mrna_for_nuclear_receptor
 x93498mrna_589-1117,mrna_for_21-glutamic_acid-rich_protein_(21-garp)_
 x93512cds_61-157:in_reversesequence,_175-211,mrna_for_telomeric_dna_binding_protein_(orf2)
 y00067mrna_2655-3207,gene_for_neurofilament_subunit_m_(nf-m)
30 y10262cds_1163-1693,eya3_gene/gb=y10262_ntype=dna_annot=cds

Metagene 453

d16481_1438-1942,mrna_for_mitochondrial_3-ketoacyl-coa_thiolase_beta-
35 subunit_of_trifunctional_protei
 d50914_1543-2077,mrna_for_kiaa0124_gene,_partial_cds_
 d82060_1801-
 2215,kidney_mrna_for_putative_membrane_protein_with_histidine_rich_charge_clusters,_comp
 d83778_4662-5154,mrna_for_kiaa0194_gene,_partial_cds_

d87443_S442-5988,mrna_for_kiaa0254_gene,_complete_cds
 hg1400-ht1400_s_at_hg1400-ht1400_carboxyl_methyltransferase,_aspartate,_altslice_1
 hg2463-ht2559_at_hg2463-ht2559_guanine_nucleotide-binding_protein_g25k_
 l06845_1728-2268,cysteinyl-tRNA_synthetase_mrna,_partial_cds_

5 l13278_1231-1753,zeta-crystallin/quinone_reductase_mrna,_complete_cds_
 l13773_8844-9252,af-4_mrna,_complete_cds_
 l21954exon_36-384:not_in_gb_record,peripheral_benzodiazepine_receptor_gene
 l25085_103-361,sec61-complex_beta-subunit_mrna,_complete_cds_
 l38961_1919-2429,putative_transmembrane_protein_precursor_(b5)_mrna,_complete_cds

10 l42572mrna_2192-2648,p87/89_gene,_complete_cds
 m14200mrna_139-469,diazepam_binding_inhibitor_(dbi)_mrna,_complete_cds
 m24400mrna_282-840,chymotrypsinogen_mrna,_complete_cds_
 m31899_2318-2708,dna_repair_helicase_(ercc3)_mrna,_complete_cds
 m64992_741-1185,prosomeal_protein_p30-33k_(pros-30)_mrna,_complete_cds

15 m65131mrna_2187-2709,methylmalonyl-coa_mutase_(mcm)_mrna,_complete_cds
 m73547_2649-3153,polyposis_locus_(dp1_gene)_mrna,_complete_cds_
 m83233_3488-3974,transcription_factor_(hf4a)_mrna,_complete_cds
 s74728_1245-1773,_antiquitin=26g_turgor_protein_homolog_[human,_kidney,_mrna,_1809_nt]
 s78569_5723-6161,_laminin_alphachain_[human,_fetal_lung,_mrna,_6204_nt]

20 u10117mrna_474-954,endothelial-monocyte_activating_polypeptide_ii_mrna,_complete_cds_
 u10439_5983-6529,double-stranded_rna_adenosine_deaminase_mrna,_complete_cds
 u12535_3273-
 3783,epidermal_growth_factor_receptor_kinase_substrate_(eps8)_mrna,_complete_cds_
 u14193_135-687,tfiia_gamma_subunit_mrna,_complete_cds

25 u15009_25-541,snrnp_core_protein_sm_d3_mrna,_complete_cds
 u26312_166-686,heterochromatin_protein_hp1hs-gamma_mrna,_complete_cds
 u28686_973-1486,putative_rna_binding_protein_rnpl_mrna,_complete_cds_
 u41654_1159-1525,adenovirus_protein_e3-14.7k_interacting_protein(fip-1)_mrna,_complete_cds
 u41740_7119-7635,trans-golgi_p230_mrna,_complete_cds_

30 u43899_2320-2740,signal_transducing_adaptor_molecule_stam_mrna,_complete_cds_
 u50523_858-1344,brca2_region,_mrna_sequence_cg037
 u50950_1546-2074,infant_brain_unknown_product_mrna,_complete_cds_
 u57099_666-1158,apeg-1_mrna,_complete_cds
 u67319_2133-2529,lice2_beta_cysteine_protease_mrna,_complete_cds.

35 u69645_551-1037,zinc_finger_protein_mrna,_complete_cds_
 u70987_1308-1830,gap_binding_protein_p62dok_(dok)_mrna,_complete_cds_
 u93237mrna#1_2162-
 2738,_men1_gene_(menin)_extracted_frommenin_(men1)_gene,_complete_cds.
 all_x12791_311-870,mrna_for_19kd_protein_of_signal_recognition_particle_(srp)

x52151cds_1148-1394:in_reversesequence,_1884-1980,arylsulphatase_a_mrna,_complete_cds
x52730mrna#1_455-911,_phenylethanolamine_n-
methyltransferase_gene_extracted_fromgene_for_phenylethan
x54326cds_4149-4299:in_reversesequence,_4363-4507,mrna_for_glutaminyl-trna_synthetase_-
5 all_x63469_962-1467,mrna_for_transcription_factor_tfiie_beta_
all_x65644_8589-9100,mrna_mbp-2_for_mhc_binding_protein_2
x75535exon#8_2216-2768,mrna_for_pxf_protein
all_x75962_913-1340,mrna_for_ox40_homologue
all_x77548_2835-3418,_hsapiens_cdna_for_rfg_
10 all_x84195_230-723,mrna_for_acylphosphatase,_muscle_type_(mt)_isoenzyme
x99296exon#1_28-
223,_rd_fromrd_gene_(5'_partial)_and_g11a_gene_(5'_partial)/gb=x99296_ntype=dna_an
all_y00264_2984-3321,mrna_for_amyloid_a4_precursor_of_alzheimer_disease
all_z22551_4012-4595,kinectin_gene_-
15 z46973cds_2460-2634:in_reversesequence,_2711-2891,mrna_for_phosphatidylinositol_3-kinase
z97074_852-1176,mrna_for_rab9_effector_p40,_complete_cds

Metagene 415

20 d83657exon#1-3_13-167:in_reversesequence,_2025:not_in_gb_record,dna_for_caafl_(calcium-binding_prote
hg4740-ht5187_at_hg4740-ht5187_transcription_factor_eb_
m64925_1400-1940,palmitoylated_erythrocyte_membrane_protein_(mpp1)_mrna,_complete_cds
u18088_1188-1742,3'_-5'_-
25 cyclic_amp_phosphodiesterase_inactive_splice_variant_hspde4a8a_mrna,_complete_cds
u22377_5634-6168,zn-15_related_zinc_finger_protein_(rlf)_mrna,_complete_cds
u41766_3235-3653,metallopeptidase/disintegrin/cysteine-rich_protein_precursor_(mdc9)_mrna,_complete_c
u43185_3667-4243,signal_transducer_and_activator_of_transcription_stat5a_mrna,_complete_cds
30 u53476_841-1351,proto-oncogene_wnt7a_mrna,_complete_cds
v00536mrna_811-1135,_ifng_gene_extracted_fromimmune_interferon_(ifn-gamma)_gene_
y00282cds_1657-1849:in_reversesequence,_2341-2383,mrna_for_ribophorin_ii

Metagene 257

35 ac002115cds#4_474-750:in_reversesequence,_100047-
100269,_cox6b_gene_(coxg)_extracted_fromdna_from_ov
af001620_1478-2000,trabecular_meshwork-
induced glucocorticoid_response_protein_(tigr)_mrna,_complete

hg4185-ht4455_at_hg4185-ht4455_estrogen_sulfotransferase,_ste
 hg537-ht537_at_hg537-ht537_collagen,_type_viii,_alpha_2
 119183mrna_1533-1959,mac30_mrna,_3'_end
 127584cds_1093-1400:in_reversesequence,_1464-
5 1677,ca_channel_b3_subunit_(cal_bet_3)_mrna,_complete_c
 l39009mrna_109-
 475,iv_alcohol_dehydrogenase(adh7)_gene,_5'_flanking_region/gb=l39009_ntype=dna_/_ann
 m10058mrna_706-1252,asialoglycoprotein_receptor_h1_mrna,_complete_cds
 m18700cds_288-784,elastase_iii_a_gene,_exon_8
10 m24122mrna_309-774,myosin_alkali_light_chain_(ventricular)_mrna,_complete_cds
 m26679exon#2_505-925,homeobox_protein_(hox-1.3)_gene,_complete_cds
 m73047_4025-4565,tripeptidyl_peptidase_ii_mrna,_complete_cds
 s67156_876-1368,_asp=aspartoacylase_[human,_kidney,_mrna,_1435_nt]
 u07225_1430-1958,p2u_nucleotide_receptor_mrna,_complete_cds
15 u18288_2804-3314,clone_ciita-10_mhc_ii_transactivator_ciita_mrna,_complete_cds_
 u19878_1137-1647,transmembrane_protein_mrna,_complete_cds
 x52479cds_1689-1995:in_reversesequence,_2040-
 2202,pkc_alpha_mrna_for_protein_kinase_c_alpha_
 x99802_1983-2463,mrna_for_zyg_homologue
20 z33642mrna_2763-3291,v7_mrna_for_leukocyte_surface_protein_

Metagene 321

all_d13315_1488-1975,mrna_for_lactoyl_glutathione_lyase
25 d14812_1345-1747,mrna_for_kiaa0026_gene,_complete_cds
 d16469_2264-2738,mrna_for_orf_xq_terminal_portion_
 d23662_61-565,mrna_for_ubiquitin-like_protein,_complete_cds
 d30756_4053-4611,mrna_for_kiaa0049_gene,_complete_cds
 d31767_1338-1812,mrna_for_kiaa0058_gene,_complete_cds
30 d50495mrna_493-1033,mrna_for_transcription_elongation_factor_s-ii,_hs-ii-t1,_complete_cds
 d86985_5502-5946,mrna_for_kiaa0232_gene,_complete_cds
 d87438_3322-3808,mrna_for_kiaa0251_gene,_partial_cds_
 hg1595-ht4788_s_at_hg1595-ht4788_heterogeneous_nuclear_ribonucleoprotein_i,_altslice_2,_ptb-
 1_
35 hg4683-ht5108_s_at_hg4683-ht5108_tumor_necrosis_factor_receptorassociated_protein_trap3_
 hg998-ht998_s_at_hg998-ht998_sulfotransferase,_phenol-preferring_
 j03805_926-1491,phosphatase_2a_mrna,_partial_cds_
 l19686mrna_61-493,macrophage_migration_inhibitory_factor_(mif)_gene,_complete_cds
 l36151_2433-2907,phosphatidylinositol_4-kinase_mrna,_complete_cds_

138810mrna_706-1246,thyroid_receptor_interactor_(trip1)_mrna,_complete_cds
 140391mrna_889-1435,(clone_s153)_mrna,_fragment
 143964_1671-2211,(clone_f-t03796)_stm-2_mrna,_complete_cds
 177213mrna_479-959,phosphomevalonate_kinase_mrna,_complete_cds
5 m34175mrna_5100-5670,beta_adaptin_mrna,_complete_cds_
 m62762_681-1083,vacuolar_h+_atpase_proton_channel_subunit_mrna,_complete_cds_
 m63959_1030-1444,alpha-2-macroglobulin_receptor-associated_protein_mrna,_complete_cds
 m69023_524-1088,globin_gene
 m98343_2695-3163,amplaxin_(ems1)_mrna,_complete_cds_
10 u02556_1579-2101,rp3_mrna,_complete_cds
 u17969exon#6_165-663,initiation_factor_eif-5a_gene,_complete_cds_
 u19796_406-760,melanoma_antigen_p15_mrna,_complete_cds_
 u22897_1798-2338,nuclear_domainprotein_(ndp52)_mrna,_complete_cds_
 u25435_3227-3737,transcriptional_repressor_(ctcf)_mrna,_complete_cds_
15 u31930_411-963,deoxyuridine_nucleotidohydrolase_mrna,_complete_cds_
 u36341mrna#1_3376-
 3862,_slc6a8_gene_(creatine_transporter)_extracted_fromxq28_cosmid,_creatine_trans
 u49869mrna_785-887,ubiquitin_gene,_complete_cds_
 u64444_633-1113,ubiquitin_fusion-degradation_protein_(ufd1l)_mrna,_complete_cds
20 u72342mrna_5025-
 5499,platelet_activating_factor_acetylhydrolase,_brain_isoform,_45_kda_subunit_(lis1
 u78095_942-1434,placental_bikunin_mrna,_complete_cds_
 u80017mrna#2_5760-
 6039,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcripti
25 u81556_1541-1925,hypothetical_protein_a4_mrna,_complete_cds
 all_x04526_2577-2968,liver_mrna_for_beta-subunit_signal_transducing_proteins_gs/gi_(beta-g)
 x13546mrna_657-1137,_puthmgi-17_protein_gene_extracted_fromhmg-17_gene_for_non-
 histone_chromosomal_pr
 x15341cds_13-235:in_reversesequence,_374-500,cox_via-l_mrna_for_cytochrome_c_oxidase_liver-
30 specific_
 all_x55330_1609-2120,mrna_for_aspartylglucosaminidase
 x56681mrna_1311-1835,jund_mrna_
 all_x64330_3792-4243,mrna_for_atp-citrate_lyase
 all_x64364_1014-1561,mrna_for_m6_antigen_
35 all_x75593_679-1202,mrna_for_rab_13
 x82103cds_660-840:in_reversesequence,_954-1128,mrna_for_beta-cop
 all_x84709_1088-1683,mrna_for_mediator_of_receptor-induced_toxicity
 z35093cds_674-842:in_reversesequence,_898-976,mrna_for_surf-1_

Metagene 473

j00219cds_110-467:in_reversesequence,_4721-4823,immune_interferon_(ifn-gamma)_gene,_complete_cds
 5 s78873_291-
 835,_mss4=zn2+_binding_protein/guanine_nucleotide_exchange_factor_[human,_brain,_mrna_partial_s83366_910-
 2840,_region_centromeric_to_t(12;17)_brakepoint:_orf1/unknown_43_amino_acid_transcrip
 y10515mrna_79-307,mrna_for_cd58_t7_protein/gb=y10515_ntype=rna
 10 z83800_115-505,mrna_for_cytoplasmic_dynein_heavy_chain_(partial,_id_hdhc11)

Metagene 470

d49677_905-1445,u2af1-rs2_mrna,_complete_cds_
 15 hg2797-ht2905_s_at_hg2797-ht2905_clathrin,_light_polypeptide_altslice_1
 122548_2914-3334,collagen_type_xviii_alpha(col18a1)_mrna,_partial_cds_
 127624_373-917,tissue_factor_pathway_inhibitor-2_mrna,_complete_cds_
 m57710_355-865,ige-binding_protein_(epsilon-bp)_mrna,_complete_cds_
 s54005_2-197,_thymosin_beta-10_[human,_metastatic_melanoma_cell_line,_mrna,_453_nt]
 20 s75295_2339-
 2915,_nucleoprotein_interactor_1=srp1_homolog_[human,_cervical_carcinoma_hela_cells,_mrna_s81578_13-271,_dioxin-
 responsive_gene_{putative_polyadenylation_signal_region}_[human,_hepatoma_g2_c
 u09410_1481-2003,zinc_finger_protein_znf131_mrna,_partial_cds
 25 u26648_936-1482,syntaxinmrna,_complete_cds
 u46025cds_2254-2710:in_reversesequence,_2777-2843,translation_initiation_factor_eif-
 3_p110_subunit_g
 all_x57348_844-1377,mrna_(clone_9112)
 all_x66087_3046-3563,a-myb_mrna
 30 all_x69433_1312-1733,mrna_for_mitochondrial_isocitrate_dehydrogenase_(nadp+)_
 x70476mrna_2526-3024,subunit_of_coatomer_complex_
 x98507cds_2790-3018:in_reversesequence,_3131-3293,mrna_for_myosin-i_beta
 y08136cds_292-496:in_reversesequence,_520-820,mrna_for_asm-like_phosphodiesterase_3a

35 Metagene 462

d88155cds_1025-1357:in_reversesequence,_439-576,dna_for_ad4bp_(sf-1)_gene_
 hg3925-ht4195_at_hg3925-ht4195_surfactant_protein_sp-a2_delta_

j02960cds#1_394-729:in_reversesequence,_1015-
 1252,_unknown_protein_gene_extracted_frombeta-2-adrener
 178833exon#24_1038-
 1476,_brca1_gene_extracted_frombrca1,_rho7_and_vati_genes,_complete_cds,_and_ipf3
5 m16937_806-1310,homeo_box_c1_protein_mrna,_complete_cds_
 all_m21064_1360-1426,migration_inhibitory_factor-related_protein(mrp14)_gene,_complete_cds_
 m76558_7124-7592,neuronal_dhp-sensitive,_voltage-dependent,_calcium_channel_alpha-
 1d_subunit_mrna,_c
 u18548exon_620-1046,gpr12_g_protein_coupled-receptor_gene,_complete_cds
10 u29195exon_927-1443,neuronal_pentraxin_ii_(nptx2)_gene_
 u32324_1353-1671,interleukin-11_receptor_alpha_chain_mrna,_complete_cds
 u92027_524-1028,clone_61501_defective_mariner_transposon_hsmar2_mrna_sequence
 all_x15218_3012-3511,ski_oncogene_mrna_
 x51954exon_10-148,ucp_gene_for_uncoupling_protein_exon/gb=x51954_ntype=dna_annot=exon_
15 x52282cds_1092-1597,mrna_for_atrial_natriuretic_peptide_clearance_receptor_(anp-c_receptor)
 all_x96698_662-1245,mrna_for_d1075-like_gene_
 y09615cds_891-1131:in_reversesequence,_1268-
 1472,mrna_for_mitochondrial_transcription_termination_fa
 y13618_7553-7895,mrna_for_dffry_protein,_abundant_transcript
20 z73677mrna_91-137,gene_encoding_plakophilin_1b.

Metagene 445

ab002314_6334-6898,mrna_for_kiaa0316_gene,_complete_cds/gb=ab002314_ntype=rna_
25 hg2600-ht2696_at_hg2600-ht2696_guanine_nucleotide-binding_protein_rap2b,_ras-
 oncogene_related
 hg2602-ht2698_at_hg2602-ht2698_succinate_dehydrogenase,_flavoprotein_subunit_
 l27586_1755-2205,tr4_orphan_receptor_mrna,_complete_cds
 all_m24748_1170-1531,_thral1_gene_(thyroid_receptor_alpha-
30 1)_extracted_fromthyroid_hormone_receptor_a
 u45983cds_789-1005:in_reversesequence,_1304-1496,g_protein-coupled_receptor_gpr-
 cy6_gene,_complete_c
 u49187_1780-2206,placenta_(diff48)_mrna,_complete_cds
 u66464_2131-2701,hematopoietic_progenitor_kinase_(hpk1)_mrna,_complete_cds_
35 u70321_1127-1643,herpesvirus_entry_mediator_mrna,_complete_cds_
 x66360cds_1134-1518:in_reversesequence,_1629-1689,mrna_pctaire-
 2_for_serine/threonine_protein_kinase
 all_x90840_6383-6942,mrna_for_axonal_transporter_of_synaptic Vesicles
 all_z80777_449-807,h2a/k_gene

Metagene 442

hg2075-ht2137_s_at_hg2075-ht2137_camp-responsive_element_modulator,_altslice_1
 5 m30135cds_139-361:in_reversesequence,_4255-4303,p40_t-
 cell_and_mast_cell_growth_factor_(hp40)_gene,_
 u13680_767-1160,lactate_dehydrogenase-c_(ldh-c)_mrna,_complete_cds_
 u66033_1937-2495,glycan-5_(gpc5)_mrna,_complete_cds
 all_x51420_2264-2781,mrna_for_tyrosinase-related_protein_
 10 x58298cds_824-1371:in_reversesequence,_1441,mrna_for_interleukin-6-receptor_

Metagene 425

ab000410mrna_947-1442,hogg1_mrna,_complete_cds_
 15 d13118_61-523:in_reversesequence,_529,mrna_for_atp_synthase_subunit_c_encoded_by_p1_gene
 d16611_1726-2299,mrna_for_coproporphyrinogen_oxidase,_complete_cds_
 d85418_875-1403,mrna_for_phosphatidylinositol-glycan-class_c_(pig-c),_complete_cds_
 d86519_1368-1932,mrna_for_neuropeptide_y/peptide_yy_y6_receptor,_complete_cds
 d87845_1946-2216,mrna_for_platelet-activating_factor_acetylhydrolase_2,_complete_cds_
 20 hg3491-ht3685_at_hg3491-ht3685_zinc_finger_protein_zfp-36
 j03925_4110-4656,mac-1_gene_encoding_complement_receptor_type_3,_cd11b,_complete_cds_
 j04970_1397-1715,carboxypeptidase_m,_3'_end
 114595_1801-2077,alanine.serine.cysteine.threonine_transporter_(asct1)_mrna,_complete_cds
 134657mrna_2757-3219,platelet/endothelial_cell_adhesion_molecule-1_(pecam-1)_gene_
 25 m28212_175-691,gtp-binding_protein_(rab6)_mrna,_complete_cds
 m55543mrna_1356-1872,guanylate_binding_protein_isoform_ii_(gbp-2)_mrna,_complete_cds_
 m55683_2732-3242,cartilage_matrix_protein_(cmp)_mrna,_exons_8-mar
 m62424_2868-3117,thrombin_receptor_mrna,_complete_cds
 m63154_977-1541,intrinsic_factor_mrna,_complete_cds
 30 m95809_1310-1850,basic_transcription_factor_62kd_subunit_(btf2),_complete_cds
 s83249_19-349,_ng-
 tra=transporter_protein/putative_hormone_extrusion_pump_[human,_liver_and_various_
 u03270_626-1136,centrin_mrna,_complete_cds_
 u20938_3946-4348,lymphocyte_dihydropyrimidine_dehydrogenase_mrna,_complete_cds.
 35 u40992_839-1175,heat_shock_protein_hsp40_homolog_mrna,_complete_cds
 u68133_4-133,scc-
 s4_mrna_expressed_in_primary_and_relatively_radiosensitive_squamous_cell_carcinoma,
 u88667_6771-7251,atp_binding_cassette_transporter_(abcr)_mrna,_complete_cds
 all_x00088_334-787,histone_h2b_gene

all_x67081_578-810,histone_h4_gene_
 x69089_4333-4849,mrna_for_skeletal_muscle_165kd_protein
 x89101exon#3_8-96:in_reversesequence,_183-188,mrna_for_fas_(apo-
 1,_cd95)/gb=x89101_ntype=rna
5 x90530cds_632-1100:in_reversesequence,_1548-1554,mrna_for_ragb_protein
 z68747cds_656-1106:in_reversesequence,_1177,mrna_for_imogen_38
 z69915mrna_31-244,mrna_(clone_icrfp50711876).

Metagene 389

10

j05125_1038-1422,triglyceride_lipase_mrna,_complete_cds
 m68840_1558-1924,monoamine_oxidase_a_(maoa)_mrna,_complete_cds_
 u85707_1922-2426,leukemogenic_homolog_protein_(meis1)_mrna,_complete_cds_
 u90916_1309-1825,clone_23815_mrna_sequence_

15

Metagene 363

hg1496-ht1496_s_at_hg1496-ht1496_adrenal-specific_protein_pg2
 s73205_2183-
20 2573,_insulin_activator_factor_[human,_pancreatic_insulinoma,_mrna_partial,_2622_nt]/gb=
 u00930_2705-3191,clone_c4e_1.63_(cac)n/(gtg)n_repeat-containing_mrna_
 x59131_2735-3119:not_in_gb_record,d13s106_mrna_for_a_highly_charged_amino_acid_sequene

Metagene 350

25

d14497_2222-2726,mrna_for_proto-oncogene_protein,_complete_cds_
 d64015_1126-1222,mrna_for_t-cluster_binding_protein,_complete_cds/gb=d64015_ntype=rna
 l00352exon_1952-2492,low_density_lipoprotein_receptor_gene_
 l07493_193-631,replication_protein_a_14kda_subunit_(rpa)_mrna,_complete_cds_
30 u20980_1596-2118,chromatin_assembly_factor-i_p60_subunit_mrna,_complete_cds
 u34962_1074-1560,transcription_factor_hcsx_(hcsx)_mrna,_complete_cds_
 u46571_1183-1687,tetratricopeptide_repeat_protein_(ptr2)_mrna,_complete_cds
 x56088mrna_2240-2794,mrna_for_cholesterol_7-alpha-hydroxylase

35

Metagene 344

m57293mrna#1_4-289,parathyroid_hormone-
 related_peptide_(pthrp)_gene,_exons_1a,_1b,_1c,_and/gb=m57293
 m85276exon#2-5_5-92:in_reversesequence,_5295:not_in_gb_record,nkg5_gene,_complete_cds_

all_x69116_2-434,znf37a_gene_for_zinc_finger_protein_
z80345mrna_4931-5457,scad_gene,_5'_utr_exonand(and_joined_cds)

Metagene 315

5

d83018_2645-3149,mrna_for_nei-related_protein_2,_complete_cds
all_l31860_2084-2589,glycophorin_mn-types_(gypa)_mrna,_complete_cds_
m16961_937-1477,alpha-2-hs-glycoprotein_alpha_and_beta_chain_mrna,_complete_cds
all_u01317_19502-63478,_epsilon-
10 globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsilon
u01877_8517-8997,p300_protein_mrna,_complete_cds_

Metagene 314

15 104656_370-856,carbonic_anhydrase_related_protein_(carp)_mrna,_complete_cds_
149209exon_25-
92,retinoblastoma_susceptibility_protein_(rb1)_i66dbp_deletion_mutant_(resulting_in_pr
m84605_4280-4766,putative_opioid_receptor_mrna,_complete_cds_
u14747_410-944,visinin-like_peptidehomolog_mrna,_complete_cds_
20 u21556_709-1204,membrane_protein-like_protein_mrna,_partial_cds/gb=u21556_/ntype=rna_
u50929_1910-2330,betaine:homocysteine_methyltransferase_mrna,_complete_cds_
u83326cds_538-1010,cc_chemokine_receptor-5_(ccr5)_gene,_complete_cds.

Metagene 259

25

m57471exon_13-59,urate_oxidase_(uox)_gene,_exon/gb=m57471_/ntype=dna/_annot=exon_
m99439_1082-1385,transducin-like_enhancer_protein_(tle4)_mrna,_3'_end
u46024_2801-3377,myotubularin_(mtm1)_mrna,_partial_cds_
all_u57341_2-
30 129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341_/ntype=rna,neurofilamen
u82468_1566-2091,tubby_related_protein(tulp1)_mrna,_complete_cds
x56741cds_85-595:in_reversesequence,_617,mrna_for_rab8_gene_
x74328mrna_1175-
1745,_cb2_(peripheral)_cannabinoid_receptor_gene_extracted_frommrna_for_cb2_(periphe

35

Metagene 232

all_d38024_2639-
3228,facioscapulohumeral_muscular_dystrophy_(fshd)_gene_region,_d4z4_tandem_repeat_u

hg2260-ht2349_s_at_hg2260-ht2349_duchenne_muscular_dystrophy_protein_(dmd)_
 hg4020-ht4290_s_at_hg4020-ht4290_transglutaminase
 m13994mrna_4482-5005,b-cell_leukemia/lymphoma(bcl-2)_proto-oncogene_mrna_encoding_bcl-2-
 alpha_protei
5 u27516_2109-2555,recombination_protein_rad52_mrna,_complete_cds
 u82970_2601-3009,metalloendopeptidase_homolog_(pex)_mrna,_complete_sequence
 x03168cds_926-1400:in_reversesequence,_1497-1509,mrna_for_s-protein_
 all_x89067_751-1136,mrna_for_trpc2_transcript_(possible_pseudogene)

10 Metagene 226

ab001325_967-1387,aqp3_gene_for_aquaporine(water_channel),_partail_cds
 all_d31784_3804-4249,mrna_for_cadherin-6_
 d42087_1034-1388,mrna_for_kiaa0118_gene,_partial_cds_

15 d87436_5660-6116,mrna_for_kiaa0249_gene,_complete_cds
 all_l32866_67-452,effector_cell_protease_receptor-1_(epr-1)_gene,_partial_cds
 all_m17262_16806-
 26862:in_m17262cds_1666,prothrombin_(f2)_gene,_complete_cds,_and_alu_and_kpni_repea
 m26692exon#1_37-195,lymphocyte-

20 specific_protein_tyrosine_kinase_(lck)_gene,_exon_1,_and_downstream_p
 m30269_4417-4849,nidogen_mrna,_complete_cds
 s55606_718-1228,_betacellulin_[human,_mrna,_1271_nt]
 u02019_1958-2462,au-rich_element_rna-binding_protein_auf1_mrna,_complete_cds_
 u18934_4229-4311,receptor_tyrosine_kinase_(dtk)_mrna,_complete_cds_

25 u58034cds_38-
 224,myotubularin_related_protein(mtmr3)_gene,_partial_cds/gb=u58034_/ntype=rna_
 u79246_1346-1748,clone_23799_mrna_sequence_
 u79289_1287-1809,clone_23695_mrna_sequence_
 x71125utr#1_20-398:in_reversesequence,_985-1093,mrna_for_glutamine_cyclotransferase_

30 all_x97261_25-333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
 x97674cds_4092-4326:in_reversesequence,_4536-
 4758,mrna_for_transcriptional_intermediary_factor_2

Metagene 188

35
 d10537_1359-1876,mrna_for_major_structural_protein_of_myelin,_complete_cds_
 d26443_3282-3822,mrna_for_glutamate_transporter,_complete_cds
 d31897_1050-1548,mrna_for_doc2_(double_c2),_complete_cds_
 d38081_2769-2853,mrna_for_thromboxane_a2_receptor,_complete_cds

d43767_43-505,mrna_for_chemokine,_complete_cds_
 d50855_2772-3309,mrna_for_ca-sensing_receptor,_complete_cds
 d63940_153-656,mrna_for_mxil_protein,_complete_cds_
 d80007_5240-5768,mrna_for_kiaa0185_gene,_partial_cds_
5
 d82344_2434-2986,mrna_for_nbphox,_complete_cds_
 d89501exon#3_206-441,pbi_gene,_complete_cds
 hg3405-ht3586_at_hg3405-ht3586_zinc_finger_protein_bzf3
 hg3495-ht3689_at_hg3495-ht3689_collagen,_type_ix,_alpha_1
 hg358-ht358_at_hg358-ht358_homeotic_protein_7,_notch_group_
10
 hg3921-ht4191_f_at_hg3921-ht4191_homeotic_protein_c6,_i
 hg3962-ht4232_at_hg3962-ht4232_sialyltransferase,_stx
 hg4069-ht4339_s_at_hg4069-ht4339_monocyte_chemotactic_protein_
 hg4318-ht4588_s_at_hg4318-ht4588_lim-domain_transcription_factor_lim-1_
 107738_717-1125,dhp-sensitive_calcium_channel_gamma_subunit_(cacnlg)_mrna,_complete_cds_
15
 107765_1443-1923,carboxylesterase_mrna,_complete_cds_
 110403_834-1254,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds_
 131881_929-1385,nuclear_factor_i-x_mrna,_complete_cds
 138517mrna_766-1228,indian_hedgehog_protein_(ihh)_mrna,_5'_end
 143338mrna_25-151,(clone_jj1a)_cadherin_mrna_fragment/gb=143338_ntype=rna
20
 143366mrna_13-157,(clone_jj1b)_cadherin_mrna_fragment/gb=143366_ntype=rna
 m15059mrna_1025-1487,fc-epsilon_receptor_(ige_receptor)_mrna,_complete_cds_(h107_epitope)
 all_m19878_1799-
 1946,calbindin_27_gene,_exonsand_2,_and_alu_repeat/gb=m19878_ntype=dna_annot=exon,
 m20203cds_242-364,neutrophil_elastase_gene_
25
 m55047_2637-3207,synaptotagmin_mrna,_complete_cds
 m55067_754-1324,47-kd_autosomal_chronic_granulomatous_disease_protein_mrna,_complete_cds_
 m59488mrna_536-1016,s100_protein_beta-subunit_gene_
 all_m60752_611-863,histone_h2a.1_(h2a)_gene,_complete_cds
 m64676mrna_1619-1892,k+_channel_subunit_gene,_complete_cds_
30
 m80647_1317-1857,thromboxane_synthase_mrna,_complete_cds
 m84371mrna_1318-1824,cd19_gene,_complete_cds
 m85247mrna_141-
 597,dopamine_d1a_receptor_gene,_complete_exon_1,_and_exon_2,_5'_end/gb=m85247_ntype=
 all_m86528_954-1357,neurotrophin-4_(nt-4)_gene,_complete_cds_
35
 m97639_3533-4037,transmembrane_receptor_(ror2)_mrna,_complete_cds
 m97675_2799-3309,transmembrane_receptor_(ror1)_mrna,_complete_cds
 m97925mrna_121-409,defensingene,_complete_cds
 s71824_2437-2881,_n-
 cam=145_kda_neural_cell_adhesion_molecule_[human_small_cell_lung_cancer_cell_li

u05659_581-1049,17beta-hydroxysteroid_dehydrogenase_typemrna,_complete_cds
 u06698_3269-3779,neuronal_kinesin_heavy_chain_mrna,_complete_cds_
 u10485_1906-2326,lymphoid-restricted_membrane_protein_(jaw1)_mrna,_complete_cds
 u11037_19-499,sel-1_like_mrna,_complete_cds
5 u11875_48-144,interleukin-
 8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb4,_partial_cds/gb=u118
 all_u12471_1014-1255,_thrombospondin-p50_gene_extracted_fromthrombospondin-
 1_gene,_partial_cds
 u16861_1076-1610,inward_rectifying_potassium_channel_mrna,_complete_cds
10 u28131_88-283,hmgi-c_chimeric_transcript_mrna,_partial_cds.
 u29700cds_1308-1644:in_reversesequence,_8352-8382,anti-
 mullerian_hormone_type_ii_receptor_precursor_
 u35340_442-868,beta_b1-crystallin_mrna,_complete_cds_
 u38227_3-411,testis-specific_hexokinase(hhk1-tb)_mrna,_partial_cds/gb=u38227/_ntype=rna
15 u45982cds_759-1035:in_reversesequence,_1110-1338,g_protein-coupled_receptor_gpr-9-
 6_gene,_complete_c
 u49742cds_744-984:in_reversesequence,_5287-5473,rhodopsin_gene,_complete_cds
 u50146mrna_39-543,typeneuropeptide_y_receptor_(npy_y2)_gene,_partial
 u62433_2748-
20 3318,nicotinic_acetylcholine_receptor_alpha4_subunit_precursor,_mrna,_complete_cds_
 u76366_4225-4720,treacher_collins_syndrome_(tcofl)_mrna,_complete_cds
 u79303_939-1479,clone_23882_mrna,_complete_cds.
 u83171_2313-2865,macrophage-derived_chemokine_precursor_(mdc)_mrna,_complete_cds_
 x05323cds_426-792:not_in_gb_record,mrc_ox-2_gene_signal_sequence
25 x14830cds_1033-1423:in_reversesequence,_1547-
 1571,mrna_for_muscle_acetylcholine_receptor_beta-subuni
 x16666cds_422-841:in_reversesequence,_894-984,hox2i_mrna_from_the_hox2_locus
 x64044cds_1066-1402:in_reversesequence,_1538-
 1592,mmrna_for_large_subunit_of_splicing_factor_u2af_
30 x71135cds_1083-1308:in_reversesequence,_1752-1977,sox3_gene
 x73113cds_2973-3339:in_reversesequence,_3430-3520,mrna_for_fast_mybp-c
 all_x74496_1967-2520,mrna_for_prolyl_oligopeptidase
 x76770mrna_1421-1931,pap_mrna
 x78710mrna_2773-3247,mtf-1_mrna_for_metal-regulatory_transcription_factor
35 all_x79200_380-600,mrna_for_syt-
 ssx,_synovial_sarcoma_translocation_junction/gb=x79200/_ntype=rna,mr
 x83572_1392-1920,arsd_mrna_
 all_x93921_942-1471,mrna_for_protein-tyrosine_phosphatase_(tissue_type:_testis)
 y09321cds_1961-2375:in_reversesequence,_2423-2501,tafii105_mrna,_partial

y09392exon#4_364-884,mrna_for_wsl-lr,_wsl-s1_and_wsl-s2_proteins_
y10141cds_56-286,dat1_gene,_partial,_vntr/gb=y10141/_ntype=dna/_annot=cds
z47038cds_267-698,partial_cdna_sequence,_clone_x101,_putative_microtubule-
associated;_protein_la_(ma)
5 z48510exon#5-7_47-6:in_reversesequence,_471,xg_mrna_(clone_fb1)/gb=z48510/_ntype=rna
z68274cds_182-
632,dna_sequence_from_cosmid_l129h7,_huntington_disease_region,_chromosome_4p16.3_cont

Metagene 182

10

d16626_2478-3006,mrna_for_histidase,_complete_cds
d84424_1603-2053,fetal_brain_mrna_for_hyaluronan_synthase,_complete_cds
hg2999-ht4756_s_at_hg2999-ht4756_thyroid_peroxidase,_altslice_2_
l31529cds_1308-1578:in_reversesequence,_1945-2053,beta1-
15 syntrophin_(snt_b1)_gene,_complete_cds_
m81650mrna_1200-1566,semenogelin_i_(semgi)_gene,_complete_cds_
u46023_4040-4544,xq28_mrna,_complete_cds_
all_z48570_1408-1991,sp17_gene_

20 Metagene 181

af000545cds_461-
983,putative_purinergic_receptor_p2y10_gene,_complete_cds/gb=af000545/_ntype=dna/_an
d79995_4440-4806,mrna_for_kiaa0173_gene,_complete_cds
25 hg2314-ht2410_at_hg2314-ht2410_4-beta-galactosyltransferase
hg2325-ht2421_at_hg2325-ht2421_retinoic_acid_receptor,_gamma_2_
j00212mrna_393-761,leukocyte_interferon_(ifn-alpha)_alpha-f_mrna,_complete_cds_
l40394mrna_1312-1750,(clone_s194)_mrna,_3'_end_of_cds_
177566mrna_1103-1655,dgs-i_mrna,_3'_end_
30 m15517cds#3_155-419:in_reversesequence,_803-
923,_ttr_gene_extracted_frommutant_prealbumin_gene_dir
m55267mrna_573-1035,ev12_protein_gene
m77235_7902-8418,cardiac_tetrodotoxin-insensitive_voltage-
dependent_sodium_channel_alpha_subunit_(hh)
35 m80899_3582-4002,novel_protein_ahnak_mrna,_partial_sequence
all_m81780_3896-
4359,_smpd1_gene_(acid_sphingomyelinase)_extracted_fromacid_sphingomyelinase_(smpd1)
m86934_1529-1973,gs1_(protein_of_unknown_function)_mrna,_complete_cds
m90820_1286-1742,rapamycin-binding_protein_(fkbp25)_mrna,_complete_cds_

s77415cds_660-948:in_reversesequence,_1449-1617,_melanocortin-
 4_receptor_[human_genomic,_1671_nt]
 u01212cds_153-411:in_reversesequence,_1715-
 1943,olfactory_marker_protein_(omp)_gene,_complete_cds
5 u03187_1505-2015,il12_receptor_component_mrna,_complete_cds
 u09607_3463-3730,jak_family_protein_tyrosine_kinase_(jak3)_mrna,_complete_cds
 u11717_3500-3743,calcium_activated_potassium_channel_(hslo)_mrna,_complete_cds_
 u12779_1685-1959,map_kinase_activated_protein_kinasemrna,_complete_cds
 all_u13061_518-1020,dehydroepiandrosterone_sulfotransferase_(std)_gene
10 u20325exon#3_57-
 477,cocaine_and_amphetamine_regulated_transcript_cart_(hcart)_gene,_complete_cds_
 u27330_1474-
 1933,alpha_(1,3)_fucosyltransferase_(fut5)_mrna,_minor_transcript_ii,_complete_cds_
 u30185_1981-2485,orphan_opioid_receptor_mrna,_complete_cds_
15 u32331_1974-2526,rig_mrna,_complete_sequence_
 u46901mrna#1_1088-1640,nacp_gene_
 u48437_1855-2293,amyloid_precursor-like_proteinmrna,_complete_cds_
 u57057cds_1239-1515:in_reversesequence,_1871-2069,wd_protein_ir10_mrna,_complete_cds
 u63312exon#1_4-199:not_in_gb_record,cosmid_ll12nc01-
20 242e1,_etv6_gene,_exons_1b_andand_partial_cds/gb
 u79266_972-1482,clone_23627_mrna,_complete_cds.
 u79302_1414-1906,clone_23855_mrna,_partial_cds.
 u80987_438-948,transcription_factor_tbx5_mrna,_complete_cds/gb=u80987_/ntype=rna_
 u82759_406-571,homeodomain_protein_hoxa9_mrna,_complete_cds
25 all_x04201_619-1073,skeletal_muscle_1.3_kb_mrna_for_tropomyosin
 x66364cds_454-814:in_reversesequence,_922,mrna_pssalre_for_serine/threonine_protein_kinase
 all_x67734_4037-4470,mrna_for_transient_axonal_glycoprotein_(tag-1)
 all_x69699_2155-2654,pax8_mrna_
 all_x83378_4940-5523,mrna_for_putative_chloride_channel
30
 Metagene 151

 ac002464cds_799-
 1345,bac_clone_rg331p03,_complete_sequence/gb=ac002464_/ntype=dna/_annot=cds_
35 d87457_1568-2060,mrna_for_kiaa0281_gene,_complete_cds
 hg4109-ht4379_at_hg4109-ht4379_olfactory_receptor_or17-30
 u31215_3797-4037,metabotropic_glutamate_receptoralpha_(mglur1alpha)_mrna,_complete_cds
 x03473cds_270-552:in_reversesequence,_1054-1150,gene_for_histone_h1(0)

x06948cds_482-680:in_reversesequence_918-1146,mrna_for_high_affinity_ige_receptor_alpha-subunit_(fc)
all_z12173_1808-2361,gns_mrna_encoding_glucosamine-6-sulphatase

5 Metagene 124

all_x00038_599-718,h4_histone_gene_

Metagene 102

10

d25215_4320-4839,mrna_for_kiaa0032_gene,_complete_cds

d86974_5077-5308,mrna_for_kiaa0220_gene,_partial_cds_

hg3123-ht3299_at_hg3123-ht3299_homeotic_protein_gbx2_

l20861_3555-4089,proto-oncogene_(wnt-5a)_mrna,_complete_cds_

15

l29339mrna_1862-2324,na+/glucose_co-transporter_(sglt1)_gene

m91083mrna_989-1469,dna-binding_protein_(hrc1)_mrna,_complete_cds

m96684_609-867,pur_(pur-alpha)_mrna,_complete_cds

s90469_1802-2300,_cytochrome_p450_reductase_[human,_placenta,_mrna_partial,_2403_nt]

u05237_2192-2570,fetal_alz-50-reactive_clone(fac1)_mrna,_complete_cds_

20

u13896_2487-3015,homolog_of_drosophila_discs_large_protein,_isoform(hdlig-

2)_mrna,_complete_cds

u47054_853-1357,putative_mono-adp-ribosyltransferase_(htmart)_mrna,_complete_cds_

u50327mrna_1463-2020,protein_kinase_c_substrate_80k-h_gene_(prkcsh)

u66615_4601-5165,swi/snf_complex_155_kda_subunit_(bafl55)_mrna,_complete_cds_

25

u79288_1035-1509,clone_23682_mrna_sequence_

all_x69878_3909-4372,flt4_mrna_for_transmembrane_tyrosine_kinase_

all_x83618_1574-1995,mrna_for_3-hydroxy-3-methylglutaryl_coenzyme_a_synthase_

x96506cds_96-441:in_reversesequence,_600-631,mrna_for_nc2_alpha_subunit_

30

Metagene 90

m16653mrna_652-742,pancreatic_elastase_iib_mrna,_complete_cds

s83513_1328-1840,_pituitary_adenylate_cyclase_activating_polypeptide_[human,_mrna,_1940_nt]

u08049exon_19-475,peripheral_myelin_protein-22_(pmp22)_gene,_non-

35

coding_exon_1a/gb=u08049/_ntype=dna

u24056_1237-1787,inward_rectifier_k+_channel_protein_(hirk2)_mrna,_complete_cds

u43885_1914-2442,grb2-associated_binder-1_mrna,_complete_cds_

z49105mrna_1064-1259,hd21_mrna_

Metagene 56

ab000467_1590-2118,_clone_res4-25,_partial_cds
d16181exon_1310-1712,pmp2_gene_for_peripheral_myelin_protein_2_

5 hg4165-ht4435_at_hg4165-ht4435_hpc-1_
117328_1400-1868,pre-t/nk_cell_associated_protein_(3cl)_mrna,_complete_cds_
l22650_84-636,early_lymphoid_activation_protein_(epag)_mrna_sequence_
m24902mrna_2694-3018,prostatic_acid_phosphatase_mrna,_complete_cds_
m82882_3023-3503,cis-acting_sequence_

10 s76617_2203-2569,_blk=protein_tyrosine_kinase_[human,_b_lymphocytes,_mrna,_2608_nt]_
s78467_987-1384,_pig-a-
ii=glycoinositol_phospholipid_anchor_synthetic_element_[human,_paroxysmal_noc
u20350_2697-3045,g_protein-coupled_receptor_v28_mrna,_complete_cds_
u46194_1466-1997,renal_cell_carcinoma_antigen_rage-4_mrna,_complete_putative_cds_

15 u66726_2378-
2846,testis_specific_rna_binding_protein_(spgyla)_mrna,_complete_cds,testis_specific_rna
u85265_7-
63,down_syndrome_critical_region(dscr1)_gene,_alternative_exon/gb=u85265_/ntype=rna_

20 Metagene 35

af012024_658-1175,integrin_cytoplasmic_domain_associated_protein_(icap-
1b)_mrna,_complete_cds/gb=af0

d23660_889-1369,mrna_for_ribosomal_protein,_complete_cds_

25 d31883_6153-6711,mrna_for_kiaa0059_gene,_complete_cds
d78361_504-942,mrna_for_ornithine_decarboxylase_antizyme,_orfand_orf_2
d86331_1281-1777,mt2-mmp_gene_for_matrix_metalloprotein,_complete_cds
hg1103-ht1103_at_hg1103-ht1103_guanine_nucleotide-binding_protein_ral,_ras-oncogene_related
hg180-ht180_at_hg180-ht180_ahnak-a_nucleoprotein_ahnak-a_

30 hg2873-ht3017_at_hg2873-ht3017_ribosomal_protein_l30_homolog
hg3362-ht3539_s_at_hg3362-ht3539_chromosomal-translocation_associated_gene_ltg19/enl_

hg3395-ht3573_s_at_hg3395-ht3573_dnaj_homolog,_alts splice_form_2
hg3549-ht3751_at_hg3549-ht3751_wilm_tumor-related_protein
hg4319-ht4589_at_hg4319-ht4589_ribosomal_protein_15

35 hg821-ht821_at_hg821-ht821_ribosomal_protein_s13_
j03592_707-1085,adp/atp_translocase_mrna,_3'_end,_clone_phat8
j04617cds_1069-1364,in_reversesequence,_3823-4030,elongation_factor_ef-1-
alpha_gene,_complete_cds_
l04483_39-272,ribosomal_protein_s21_(rps21)_mrna,_complete_cds_

106499mrna_4-301,ribosomal_protein_l37a_(rpl37a)_mrna,_complete_cds_
 106505mrna_259-553,ribosomal_protein_l12_mrna,_complete_cds
 107868_4919-5429,receptor_tyrosine_kinase_(erbB4)_gene,_complete_cds
 111566_77-521,ribosomal_protein_l18_(rpl18)_mrna,_complete_cds
5 all_m10277_3236-3578,cytoplasmic_beta-actin_gene,_complete_cds_
 m17886mrna_7-475,acidic_ribosomal_phosphoprotein_p1_mrna,_complete_cds_
 m18000cds_78-360,ribosomal_protein_s17_gene,_complete_cds
 m19828exon#8_1305-1576:in_reversesequence,_14367-14518,apolipoprotein_b-100_(apob)_gene_
 m24194mrna_504-
10 1023,mhc_protein_homologous_to_chicken_b_complex_protein_mrna,_complete_cds_
 all_m31520_25-
 590,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_
 m31520mma_2-
 106,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_
15 m36072_368-770,ribosomal_protein_l7a_(surf_3)_large_subunit_mrna,_complete_cds_
 m55409_556-1069,pancreatic_tumor-related_protein_mrna,_3'_end
 m58603_3120-3600,nuclear_factor_kappa-b_dna_binding_subunit_(nf-kappa-
 b)_mrna,_complete_cds
 m60854_19-373,ribosomal_protein_s16_mrna,_complete_cds_
20 m64098_3873-4305,high_density_lipoprotein_binding_protein_(hbp)_mrna,_complete_cds_
 m64716mrna_31-451,ribosomal_protein_s25_mrna,_complete_cds_
 m81757_49-421,s19_ribosomal_protein_mrna,_complete_cds_
 s79522_19-481,_ubiquitin_carboxyl_extension_protein_[human,_mrna,_540_nt]_
 u07804_1857-2384,dna_topoisomerase_i_mrna,_partial_cds_
25 u07806_2865-3382,camptothecin_resistant_clone_cem/c2_dna_topoisomerase_i_mrna,_partial_cds_
 u09953_153-621,ribosomal_protein_l9_mrna,_complete_cds_
 u14968_133-451,ribosomal_protein_l27a_mrna,_complete_cds_
 u14969_43-451,ribosomal_protein_l28_mrna,_complete_cds_
 u14971_91-661,ribosomal_protein_s9_mrna,_complete_cds
30 u14973_13-235,ribosomal_protein_s29_mrna,_complete_cds_
 u25789_19-481,ribosomal_protein_l21_mrna,_complete_cds_
 u49352_548-1106,liver_2,4-dienoyl-coa_reductase_mrna,_complete_cds_
 u49785_311-641,d-dopachrome_tautomerase_mrna,_complete_cds.
 u78027mrna#3_3-350,_1441_gene_(144-
35 like_ribosomal_protein)_extracted_frombruton_tyrosine_kinase_(btk
 u79273_851-1127,clone_23933_mrna_sequence
 u83461_1235-
 1619,putative_copper_uptake_protein_(hcrt2)_mrna,_complete_cds/gb=u83461_/ntype=rna

x01677cds_629-983:in_reversesequence,_1109-1229,mrna_for_glyceraldehyde-3-phosphate_dehydrogen
x03342cds_51-375:in_reversesequence,_439-445,mrna_for_ribosomal_protein_l32_
x06617mrna_31-475,mrna_for_ribosomal_protein_s11_
5 x16064cds_147-483:in_reversesequence,_625-
745,mrna_for_translationally_controlled_tumor_protein_
x17206cds_111-585:in_reversesequence,_885,mrna_for_llrep3_
x52966cds_11-299:in_reversesequence,_19-373,mrna_for_ribosomal_protein_l35a_
x55715cds_228-618:in_reversesequence,_748-784,hums3_mrna_for_40s_ribosomal_protein_s3_
10 x56932cds_114-576:in_reversesequence,_611-623,mrna_for_23_kd_highly_basic_protein_
x56997mrna#1_19-475:not_in_gb_record,uba52_gene_coding_for_ubiquitin-
52_amino_acid_fusion_protein
all_x64707_401-888,bbc1_mrna_
x67247mrna_116-662,rps8_gene_for_ribosomal_protein_s8_
15 x69150mrna_25-403,_l06432mrna_for_ribosomal_protein_s18
x79234cds_115-511,mrna_for_ribosomal_protein_l11_
z26876_43-328,gene_for_ribosomal_protein_l38_
z28407cds_220-703:in_reversesequence,_809-818,mrna_for_ribosomal_protein_l8_
z49148cds_2-418:in_reversesequence,_18-589,mrna_for_ribosomal_protein_l29_
20 z69043cds_66-489:in_reversesequence,_30-598,mrna_translcon-
associated_protein_delta_subunit_precurs
all_z70759_4-251,mitochondrial_16s_rRNA_gene_(partial).

Metagene 2

25 d13633_2141-2597,mrna_for_kiaa0008_gene,_complete_cds
l19783_895-1351,gpi-h_mrna,_complete_cds_
l33262_1751-2273,dna_repair_and_recombination_homologue_(rad52)_gene,_complete_cds
m29927exon_229-703,ornithine_aminotransferase_gene_
30 u09087_2090-2543,thymopoietin_beta_mrna,_complete_cds
u67611_788-
1130:not_in_gb_record,_mouse_transaldolase_gene_mrna,_complete_cds/gb=u67611_/ntype=ma_
u72936_9836-
10377,putative_dna_dependent_atpase_and_helicase_(atrX)_mrna,_alternatively_spliced_prod
35 all_x67491_839-1137,gene_for_glutamate_dehydrogenase_
x99586cds_12-223:in_reversesequence,_329,mrna_for_smt3c_protein_
z46629mrna_3352-3730,sox9_mrna

Metagene 1

l00137cds#1_6-234:in_reversesequence,_8-
134:not_in_gb_record,_ghrf_gene_(growth_hormone_releasing_fa
m33478mrna_653-1049,33-kda_phototransducing_protein_mrna,_complete_cds_
5 all_m34344_114-364:in_m34344cds_3032-3069,platelet_glycoprotein_iib_(gpiib)_gene
m62810_1350-1818,mitochondrial_transcription_factormrna,_complete_cds_
m73239mrna_2114-2638,(clone_sf1)_hepatocyte_growth_factor_(hgf)_mrna,_complete_cds_
m81758_7258-7798,skeletal_muscle_voltage-
dependent_sodium_channel_alpha_subunit_(skm1)_mrna,_complet
10 all_u51561_10617-28244:in_u51561cds_50,cosmid_n79e2,_complete_sequence
u75309_1813-2376,tbp-associated_factor_(htafii100)_mrna,_partial_cds_
u95090mrna_2166-2418:in_fullsequence,_36716-
36854,chromosomecosmid_f19541,_complete_sequence
all_x13766_14-551,beta-casein_mrna_3'-terminal_fragment_

15

Metagene 434

all_m26665_267-307,histatin(his2)_mrna,_complete_cds,histatin(his2)_mrna,_complete_cds
m28130mrna_654-1002,interleukin(il8)_gene,_complete_cds
20 m33684cds_288-788,(clone_lambda-10-2)_non-receptor_tyrosine_phosphatase(ptpn1)_gene_
u10492_1894-2266,mox1_protein_(mox1)_mrna,_complete_cds
u18985_2460-2922,triadin_mrna,_complete_cds
u48213mrna_1031-1601,d-site_binding_protein_gene,_promoter_region_and

25

Metagene 408

d42039_3568-4074,mrna_for_kiaa0081_gene,_partial_cds_
d55643_443-1019,spleen_pabl_(pseudoautosomal_boundary-
like_sequence)_mrna,_clone_sp2/gb=d55643_/ntyp
30 hg3993-ht4263_at_hg3993-ht4263_cpg-enriched_dna,_clone_s12_
102785_2412-2790,colon_mucosa-associated_(dra)_mrna,_complete_cds_
m28826_976-1252,thymocyte_antigen_cd1b_mrna,_complete_cds

35

Metagene 211

ab006190_705-1179,mrna_for_aquaporin_6,_complete_cds/gb=ab006190_/ntype=rna_
d13642_4248-4722,mrna_for_kiaa0017_gene,_complete_cds
d31815_797-1295,mrna_for_smp-30_(senescence_marker_protein-30),_complete_cds_

d31846exon#4_179-713,gene_for_aquaporin-2_water_channel,_exon1-4,_complete_cds_
d38305_701-1181,mrna_for_tob,_complete_cds_
d63482_1722-2226,mrna_for_kiaa0148_gene,_complete_cds
d82070_285-843,ac1_mrna,_complete_cds

5 d85527_37-349,mrna_for_lim_domain,_partial_cds/gb=d85527_/ntype=rna
d87460_2023-2503,mrna_for_kiaa0270_gene,_partial_cds_
d87468_2496-2886,mrna_for_kiaa0278_gene,_partial_cds_
hg1649-ht1652_at_hg1649-ht1652_elastase_
hg1800-ht1823_at_hg1800-ht1823_ribosomal_protein_s20_

10 hg2261-ht2352_at_hg2261-ht2352_antigen,_prostate_specific,_alts splice_form_3
hg2604-ht2700_at_hg2604-ht2700_pan-2_
hg3432-ht3618_at_hg3432-ht3618_fibroblast_growth_factor_receptor_k-sam,_alts splice_1
hg3987-ht4257_at_hg3987-ht4257_cpg-enriched_dna,_clone_e06_
hg4036-ht4306_at_hg4036-ht4306_retinoblastoma_

15 hg4051-ht4321_at_hg4051-ht4321_choline_acetyltransferase_
hg4662-ht5075_at_hg4662-
ht5075_omega_light_chain,_immunoglobulin_lambda_light_chain_related
hg896-ht896_at_hg896-ht896_thrombospondin_
hg919-ht919_at_hg919-ht919_dna_polymerase,_epsilon,_catalytic_subunit

20 all_k03460_3-379,alpha-tubulin_isotype_h2-alpha_gene,_last_exon
l20965_3164-3680,phosphodiesterase_mrna,_complete_cds
l23852mrna_1122-1674,(clone_z146)_retinal_mrna,_3'_end_and_repeat_region
l36720_661-1219,bystin_mrna,_complete_cds_
142621mrna_1775-2231,ly-9_mrna,_complete_cds

25 l77561mrna_583-1093,dgs-d_mrna,_3'_end
all_m13903_1676-2031,involucrin_mrna_
m27749_245-323,immunoglobulin-related_14.1_protein_mrna,_complete_cds,immunoglobulin-related_14.1_pr
m30185mrna_1234-1666,cholesteryl_ester_transfer_protein_mrna,_complete_cds_

30 m34079_830-1298,immunodeficiency_virus_tat_transactivator_binding_protein-1_(tbp-1)_mrna,_complete_c
m34182mrna#1_1112-1517,testis-specific_protein_kinase_gamma-subunit_mrna,_complete_cds_
s76992_2182-2710,_vav2=vav_oncogene_homolog_[human,_fetal_brain,_mrna_partial,_2753_nt]
s78771_1149-1661,_nat=cpg_island-associated_gene_[human,_mrna,_1741_nt]
35 s81003_130-640,_1-
ubc=ubiquitin_conjugating_enzyme_[human,_odontogenic_keratocysts,_mrna_partial,_68
u01157_2506-2992,glucagon-like_peptide-1_receptor_mrna_with_ca_dinucleotide_repeat,_complete_cds_
u01922_405-921,btk_region_clone_fci-12_mrna

u08336_368-872,basic_helix-loop-helix_transcription_factor_mrna,_complete_cds
 u09210_1910-2396,vesicular_acetylcholine_transporter_mrna,_complete_cds
 u20908cds_13-193,clone_350/2_melanoma_ubiquitous_mutated_protein_(mum-
 1)_gene,_partial_cds/gb=u20908
5 u31903_2052-2510,creb-rp_(creb-rp)_mrna,_complete_cds
 u34880_1699-2179,dph2l_mrna,_complete_cds
 u37673_2848-3412,neuron-
 specific Vesicle_coat_protein_and_cerebellar_degeneration_antigen_(beta-nap)
 u39576_2486-2852, butyrophilin_precursor_mrna,_complete_cds_
10 u49089_2571-3075,neuroendocrine-dlg_(ne-dlg)_mrna,_complete_cds
 u52696_703-742,adrenal_creb-rp_homolog_(creb-rp),_complete_cds,_and_tenascin-
 x_(xb),_partial_cds,_mr
 u59302_4047-4617,steroid_receptor_coactivator-1_f-src-1_mrna,_complete_cds_
 u62317mrna#3_1056-
15 1488,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
 u66059cds#21_49-283:in_reversesequence,_207121-207343,germline_t-
 cell_receptor_beta_chain_dopamine-b
 u73328_918-1314,dlx7_(dlx7)_mrna,_complete_cds_
 u76764_2544-3054,cd97_mrna,_complete_cds_
20 u78521_655-1111,immunophilin_homolog Ara9_mrna,_complete_cds
 u78678_191-683,thioredoxin_mrna,_nuclear_gene_encoding_mitochondrial_protein,_complete_cds_
 u79258_861-1407,clone_23732_mrna,_partial_cds
 u81001_2773-3039,snrpn_mrna,_3'_utr,_partial_sequence
 u90543_2445-
25 2739,butyrophilin_(btfl)_mrna,_complete_cds,butyrophilin_(btfl)_mrna,_complete_cds
 u96629mrna#2_3194-
 3722,_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_clon
 all_x14085_1251-1422,mrna_for_beta-1,4-galactosyltransferase_(ec_2.4.1.22)_
 all_x62573_1608-2161,rna_for_fc_receptor,_tc9
30 all_x66785_2930-3511,mrna_for_transacylase_(dbt)_
 all_x78817_2647-3236,partial_c1_mrna_
 all_x83368_4789-5345,mrna_for_phosphatidylinositolkinase_gamma
 x96401_1673-2186,mrna_for_rox_protein
 x96924mrna_1184-1215,gene_encoding_mitochondrial_citrate_transport_protein
35 all_x99133_5342-5685:in_x99133cds_563-597:not_in_gb_record,ngal_gene_
 z31560cds_475-923:in_reversesequence,_953,sox-2_mrna_(partial)

ab000450_1298-1730,mrna_for_vrk2,_complete_cds_
 ab000464_3281-3743,_clone_res4-24a,_exon_1,_2,_3,_4_
 ab001106_3542-4088,mrna_for_glia_maturation_factor,_complete_cds_
 d00723_642-
5 1110,mrna_for_hydrogen_carrier_protein,_a_component_of_an_enzyme_complex,_glycine_synthas
 d11151exon_1936-2434,dna_for_endothelin-a_receptor,_5'_flanking_region_and_
 d12625_2036-2219,mrna_for_nf1_protein_isoform_(neurofibromin_isoform),_complete_cds
 d12676_1884-2220,mrna_for_lysosomal_sialoglycoprotein,_complete_cds
 d13635_4583-5117,mrna_for_kiaa0010_gene,_complete_cds
10 d13789_1594-2062,mrna_for_n-acetylglucosaminyltransferase_iii,_complete_cds
 d14662_1082-1592,mrna_for_kiaa0106_gene,_complete_cds
 d21163_3183-3693,mrna_for_kiaa0031_gene,_complete_cds
 d86549_609-969,mrna_for_p97_homologous_protein,_partial_cds
 d88532_3016-3328,mrna_for_p55piK,_complete_cds_-
15 104733_1785-2265,kinesin_light_chain_mrna,_complete_cds_
 108488_1206-1644,inositol_polyphosphate_1-phosphatase_mrna,_complete_cds_
 113434_2304-2850,chromosome_3p21.1_gene_sequence,_complete_cds_
 122009_1642-2056,hnrrnp_h_mrna,_complete_cds
 127476_3901-4429,x104_mrna,_complete_cds_-
20 138933mrna_883-
 1393,_the_longest_open_reading_frame_predicts_a_protein_of_202_amino_acids,_with_fair
 141939mrna_3197-3731,(clone_fbk_iii_11c)_protein-tyrosine_kinase_(drt)_mrna,_complete_cds_
 m37190mrna_1220-1796,ras_inhibitor_mrna,_3'_end
 all_m54968_5180-5775,k-ras_oncogene_protein_mrna,_complete_cds_-
25 m64936_2808-3264,retinoic_acid-inducible_endogenous_retroviral_dna
 m91029exon#3_2581-2977,amp_deaminase_(ampd2)_mrna_
 s59049_786-1314,_bl34=b_cell_activation_gene_[human,_mrna,_1398_nt]_
 s73149mrna_293-827,_insulin-
 like_growth_factor_ii_{intron_7}_[human,_genomic,_1702_nt]/gb=s73149_nt
30 u08023_3037-3529,cellular_proto-oncogene_(c-mer)_mrna,_complete_cds
 u08316_1719-2235,insulin-stimulated_protein_kinase(ispk-1)_mrna,_complete_cds_
 u15782_2237-2681,cleavage_stimulation_factor_77kda_subunit_mrna,_complete_cds
 u23028_1702-2236,eukaryotic_initiation_factor_2b-epsilon_mrna,_partial_cds_
 u39487_3877-4339,xanthine_dehydrogenase/oxidase_mrna,_complete_cds_-
35 u85658_2310-2736,transcription_factor_erf-1_mrna,_complete_cds_
 x62083_3969-4029,mrna_for_drosophila_female_sterile_homeotic_(fsh)_homologue_
 all_x69962_4188-4308,fmr-1_mrna
 all_x82125_2007-2368,hok-2_mrna_for_zinc_finger_protein

Metagene 143

d14663_785-1259,mrna_for_kiaa0107_gene,_complete_cds_
d38496_3615-4170,mrna_for_lztr-1,_complete_cds_

5 d42084_2112-2610,mrna_for_kiaa0094_gene,_partial_cds_
d49400_115-655,fetus_brain_mrna_for_vacuolar_atpase,_complete_cds
d84294mrna_8552-9020,mrna_for_tprdi,_complete_cds
d86988_4716-5220,mrna_for_kiaa0221_gene,_complete_cds
d87445_6334-6892,mrna_for_kiaa0256_gene,_complete_cds

10 hg1322-ht5143_s_at_hg1322-ht5143_small_nuclear_ribonucleoprotein,_polypeptide_altslice_2_
hg3484-ht3678_s_at_hg3484-ht3678_protein_kinase
j04794mrna_567-1071,aldehyde_reductase_mrna,_complete_cds
l09209_3114-3666,amyloid_protein_homologue_mrna,_complete_cds_
l35249mrna_2225-2690,vacuolar_h+-atpase_mr_56,000_subunit_(ho57)_mrna,_complete_cds_

15 l49380mrna_2916-3414,clone_b4_transcription_factor_zfm1_mrna,_complete_cds
m14483mrna_41-443,_ptma_gene_extracted_fromprothymosin_alpha_mrna,_complete_cds_
m26708_549-1008,prothymosin_alpha_mrna_(prot-alpha),_complete_cds
m91432mrna_1664-2144,medium-chain_acyl-coa_dehydrogenase_(mcad)_gene_
u00115_3001-3451,zinc-finger_protein_(bcl-6)_mrna,_complete_cds

20 u09825_3156-3522,acid_finger_protein_mrna,_complete_cds
u22970mrna#1_205-749,_16-jun_gene_(interferon-
inducible_peptide_precursor)_extracted_frominterferon-
u26424_2237-2735,ste20-like_kinase_(mst2)_mrna,_complete_cds_
u45328_591-1079,ubiquitin-conjugating_enzyme_(ube2i)_mrna,_complete_cds

25 u60061_905-1325,fez2_mrna,_partial_cds_
u61397_875-1173,ubiquitin-homology_domain_protein_pic1_mrna,_complete_cds
u80017mrna#3_892-
1444,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcriptio
u91930_4196-4682,ap-3_complex_delta_subunit_mrna,_complete_cds_

30 u91931_3081-3489,ap-3_complex_beta3a_subunit_mrna,_complete_cds
u91932_778-1210,ap-3_complex_sigma3a_subunit_mrna,_complete_cds
u92014_817-1366,clone_121711_defective_mariner_transposon_hsmar2_mrna_sequence_
all_x03484_2418-2947,mrna_for Raf_oncogene_
x60787mrna_2434-3000,mrna_for_transcription_factor_ilf_

35 all_x62534_726-1137,hmg-2_mrna_
all_x63692_4825-5348,mrna_for_dna_(cytosin-5)-methyltransferase
x65784cds_58-399,car_gene
all_x66899_1902-2323,ews_mrna
x69838cds_2756-2924:in_reversesequence,_3043-3331,mrna_for_g9a

all_x69910_2339-2892,p63_mrna_for_transmembrane_protein
 all_x70394_2591-3156,ozf_mrna
 all_x72889_5441-5844,hbrm_mrna_
 all_x73478_2042-2637,hptpa_mrna
5 all_x79536_1005-1156,mrna_for_hnrnpcore_protein_a1.
 all_x86691_5882-6399,mrna_for_218kd_mi-2_protein_
 all_x89750_1061-1512,mrna_for_tgif_protein_
 all_x95404_482-1047,mrna_for_non-muscle_type_cofilin_
 x95735_1628-2168,mrna_for_zyxin_2
10 all_x98743_2619-3112,mrna_for_rna_helicase_(myc-regulated_dead_box_protein)
 all_y00815_7107-7684,mrna_for_lca-homologlar_protein_(leukocyte_antigen_related)_
 all_y08614_3715-4118,mrna_for_crm1_protein_
 all_z24724_1263-1840,polya_site_dna
 z26491exon#5_388-430,gene_for_catechol_o-methyltransferase_
15 all_z29505_1140-1468,mrna_for_nucleic_acid_binding_protein_sub2.3

Metagene 108

ab003102_956-1442,mrna_for_proteasome_subunit_p44.5,_complete_cds
20 d14659_648-1134,mrna_for_kiaa0103_gene,_complete_cds_
 d21260_5600-6002,mrna_for_kiaa0034_gene,_complete_cds
 d31885_1773-2169,mrna_for_kiaa0069_gene,_partial_cds_
 d38551_3082-3592,mrna_for_kiaa0078_gene,_complete_cds
 d38555_3911-4421,mrna_for_kiaa0079_gene,_complete_cds
25 d64142mrna_625-1177,mrna_for_histone_h1x,_complete_cds_
 d78129_568-
 1024,adult_(34_year_old)_male_liver_mrna_for_squalene_epoxidase,_partial_cds/gb=d78129/_n
 d85429exon#3_813-1347,dna_for_heat_shock_protein_40,_complete_cds
 d86972_4190-4610,mrna_for_kiaa0218_gene,_complete_cds
30 d87120_1936-2314,cancellous_bone_osteoblast_mrna_for_gs3786,_complete_cds
 hg2788-ht2896_at_hg2788-ht2896_calcyclin_
 hg2874-ht3018_at_hg2874-ht3018_ribosomal_protein_l39_homolog_
 l09604_339-819,differentiation-dependent_a4_protein_mrna,_complete_cds
 l19779_7-496,histone_h2a.2_mrna,_complete_cds_
35 l38928mrna_274-832,5,10-methenyltetrahydrofolate_synthetase_mrna,_complete_cds
 l42542mrna_3353-3803,rlip76_protein_mrna,_complete_cds_
 m31642mrna_802-1288,hypoxanthine_phosphoribosyltransferase_(hprt)_mrna,_complete_cds_
 m58460_1311-1490,75-kd_autoantigen_(pm-sc1)_mrna,_complete_cds_
 all_m59830_2432-2661,mhc_iii_hsp70-2_gene_(hla),_complete_cds

m60922_1971-2427,surface_antigen_mrna,_complete_cds
 all_m90516_2559-3058,glutamine:fructose-6-
 phosphate_amidotransferase_(gfat)_mrna,_complete_cds_
 u76992_2137-2533,tat-sfl_mrna,_complete_cds
5 x55079mrna_3257-3366:not_in_gb_record,_gaa_gene_extracted_fromlysosomal_alpha-
 glucosidase_gene_exon_
 x57985mrna#1_1652-
 2168,_gl105_gene_(histone_h2b)_extracted_fromgenes_for_histones_h2b.1_and_h2a_
 y07867cds_643-787:in_reversesequence,_1087-1237,mrna_for_pirin,_isolate_1_-

10

Metagene 50

d10667_2830-3307,mrna_for_smooth_muscle_myosin_heavy_chain_
 m72885mrna_207-750,_g0s2_gene_extracted_fromgos2_gene,_5'_flank_and_cds_
15 all_u22028_8029-
 8330,cytochrome_p450_(cyp2a13)_gene,_complete_cds,cytochrome_p450_(cyp2a13)_gene,_co
 u92459_2702-3194,metabotropic glutamate_receptormrna,_complete_cds

Metagene 18

20

u39231_1739-1979,gip_receptor_(gipr)_mrna,_complete_cds
 all_v00503_2330-2452,mrna_encoding_pro-alpha-2_chain_of_type_i_procollagen(major_part)_
 all_x79200_380-600,mrna_for_syt-
 ssx,_synovial_sarcoma_translocation_junction/gb=x79200_/ntype=rna,mr

25

Metagene 13

all_d32001_61-294,husaa1g_gene_for_serum_amyloid_a1_gamma,_exonand_intron_3_-
 hg2059-ht2114_at_hg2059-ht2114_arrestin,_beta_2
30 hg2480-ht2576_at_hg2480-ht2576_fmlp-related_receptor_i_-
 hg2809-ht2920_s_at_hg2809-ht2920_lung_surfactant_protein_d_-
 hg3107-ht3283_s_at_hg3107-ht3283_plasma_membrane_calcium_pump_hpmca2a
 hg759-ht759_s_at_hg759-ht759_adrenergic_receptor,_beta_1_-
 j05036mrna_1546-2119,cathepsin_e_mrna,_complete_cds
35 j05073cds_239-641,phosphoglycerate_mutase_(pgam-m)_gene,_complete_cds
 k02766_2028-2436,complement_component_c9_mrna,_complete_cds
 l29008_2014-2464,l-iditol-2_dehydrogenase_mrna,_complete_cds_-
 l33477_3692-4142,(clone_8b1)_br-cadherin_mrna,_complete_cds
 l35592mrna#1_1633-2107,germline_mrna_sequence_-

137112mrna_1710-1816,vasopressin_v3_receptor_mrna,_complete_cds_
 140933cds_1218-1470:in_reversesequence,_1639-1819,phosphoglucomutase-
 related_protein_(pgmrp)_gene,_c
 all_m80333_1628-2079,m5_muscarinic_acetylcholine_receptor_gene,_complete_cds_
5 m85217_2529-2955,k+_channel_protein_(hlk3)_mrna,_complete_cds
 m89473_1394-1706,neurokininreceptor_(nk3r)_mrna,_complete_cds_
 m96859_3150-3630,dipeptidyl_aminopeptidase_like_protein_mrna,_complete_cds_
 u09609_2198-2708,p80ht_(p80ht/nkfb-2)_mrna,_complete_cds_
 u13737_2046-2556,cysteine_protease_cpp32_isoform_alpha_mrna,_complete_cds
10 u14910_910-1360,rpe-retinal_g_protein-coupled_receptor_(rgr)_mrna,_complete_cds
 u18671mrna_2702-3266,stat2_gene,_complete_cds_
 u29615_1098-1530,chitotriosidase_precursor_mrna,_complete_cds
 u31929cds_1063-1361:in_reversesequence,_6372-
 6576,orphan_nuclear_receptor_(dax1)_gene,_complete_cds_
15 u63336_1666-2062,mhc_i_region_proline_rich_protein_mrna,_complete_cds
 u65404_1140-1530,erythroid-specific_transcription_factor_eklf_mrna,_complete_cds.
 u78180_3340-3880,sodium_channel(hbnac2)_mrna,_alternatively_spliced,_complete_cds_
 u85992_1236-1596,clone_image:35527_unknown_protein_mrna,_partial_cds_
 all_u87408_1441-1952,clone_image:74593_unknown_protein_mrna,_partial_cds_
20 v00535mrna#1_253-692,_interferon_beta gene_extracted_from_gene_for_fibroblast_interferon_beta_1
 all_x04729_2-263,mrna_for_plasminogen_activator_inhibitor_typen-
 terminus/gb=x04729_ntype=rna_
 x54816_at_x54816_x54816,not_in_gb_record,gene_for_alpha-1-microglobulin-bikunin,_exons_5-
 jan_(encodi
25 all_x54938_1175-1752,mrna_for_inositol_1,4,5-triphosphate_3-kinase_
 x55889cds_264-546:not_in_gb_record,gene_for_ciliary_neurotrophic_factor,_exon_1_
 x55990mrna_163-489,epc_gene_for_eosinophil_cationic_protein_
 all_x66141_261-784,mrna_for_cardiac_ventricular_myosin_light_chain-2_
 x97748mrna_59-189,ptx3_gene_promotor_region/gb=x97748_ntype=dna_annot=mrna_
30 all_x99140_1407-1822,mrna_for_hair_keratin,_hhb5_
 y10376cds_888-1158:in_reversesequence,_1222-1408,mrna_for_sirp-beta1_
 y13115cds_2477-2879:in_reversesequence,_3061,mrna_for_serine/threonine_protein_kinase_sak
 z24680mrna_3558-4044,garp_gene_mrna,_complete_cds
 all_z31357_967-1502,mrna_for_cysteine_dioxygenase_type_1_
35
 Metagene 486

all_m60751_910-1163,histone_h2b.1_(h2b)_gene,_complete_cds_
 x81333cds_1730-2078:in_reversesequence,_2130-2220,mrna_for_pph_beta_subunit_protein_

all_y00317_1618-2081,mrna_for_liver_microsomal_udp-glucuronosyltransferase_(udpgt)_

Metagene 397

5 u91618_167-671,proneurotensin/proneuromedin_n_mrna,_complete_cds.
 x78121mrna_1730-1940:in_reversesequence,_1970-2036,mrna_for_choroideremia_
 y07828cds_345-675:in_reversesequence,_844-994,mrna_for_ring_protein_

Metagene 373

10 d26350_10043-10481,mrna_for_typeinositol_1,4,5-trisphosphate_receptor,_complete_cds_
 hg4747-ht5195_at_hg4747-ht5195_nadh-ubiquinone_oxidoreductase,_51_kda_subunit
 m22612_188-759,pancreatic_trypsin(try1)_mrna,_complete_cds
 all_x74008_1842-2245,mrna_for_protein_phosphatasegamma

15

Metagene 356

d26156_4588-5166,mrna_for_transcriptional_activator_hsnf2b,_complete_cds_
 d86964_5449-5995,mrna_for_kiaa0209_gene,_partial_cds_
 20 hg3141-ht3317_f_at_hg3141-ht3317_nadh-ubiquinone_oxidoreductase,_39_kda_subunit
 k03494cds_557-1062:in_reversesequence,_115,green_cone_photoreceptor_pigment_gene_1
 119437_857-1211,transaldolase_mrnaContaining_transposable_element,_complete_cds_
 l24783_78-624,mrna_fragment/gb=l24783_/ntype=rna
 l28010_1292-1748,hnrnp_f_protein_mrna,_complete_cds_
 25 m80254_492-840,cyclophilin_isoform_(hcyp3)_mrna,_complete_cds
 m88108_2156-2636,p62_mrna,_complete_cds
 u19251_s_at_u19251_u19251,not_in_gb_record,neuronal_apoptosis_inhibitory_protein_mrna,_comp
 lete_cds
 u24166_2107-2395,eb1_mrna,_complete_cds
 30 u33936_578-1050,adenosine_kinase_mrna,_complete_cds/gb=u33936_/ntype=rna_
 u51990_867-1269,hprp18_mrna,_complete_cds
 u60521_1398-1860,protease_promch6_(mch6)_mrna,_complete_cds
 u62389_31-409,putative_cytosolic_nadp-
 dependent_isocitrate_dehydrogenase_mrna,_partial_cds/gb=u62389
 35 u72511_440-596,b-cell_receptor_associated_protein_(hbap)_mrna,_partial_cds_
 x05196exon#9_2-458:in_reversesequence,_3199:not_in_gb_record,aldolase_c_gene_
 all_x12953_859-1130,rab2_mrna,_ypt1-related_and_member_of_ras_family_
 all_x17644_1976-2559,gst1-hs_mrna_for_gtp-binding_protein
 x57152mrna#1_536-962,gene_for_casein_kinase_ii_subunit_beta_(ec_2.7.1.37)_

x78338mrna_5278-5824,_synthetic_adenovirus_transformedretina_cell_line,_mrp_mrna_all_x91247_3261-3700,mrna_for_thioredoxin_reductase

x97065cds_1852-2260:in_reversesequence,_2389-2395,mrna_for_sec23b_isoform,_2450bp_x98411cds_2016-2256:in_reversesequence,_2340-2490,mrna_for_myosin-ie

5 x99209_1549-2053,mrna_for_arginine_methyltransferase_all_z11695_2189-2736,40_kda_protein_kinase_related_to_rat_erk2_z29481cds_624-792:in_reversesequence,_898-1186,mrna_for_3-hydroxyanthranilic_acid_dioxygenase

10 Metagene 154

d00408_1373-1921,fetal_liver_cytochrome_p-450_(p-450_hfla),_complete_cds,fetal_liver_cytochrome_p-45

d13638_5003-5557,mrna_for_kiaa0013_gene,_complete_cds

15 hg2320-ht2416_at_hg2320-ht2416_integrin,_betasubunit
m24351_cds2_at_m24351_m24351,not_in_gb_record,_pthlh_gene_(parathyroid_hormone-like_protein_a)_extra
m73489_3312-3660,heat-stable_enterotoxin_receptor_mrna,_complete_cds_u73330exon_13-77,pac_85d2,_complete_sequence/gb=u73330_/ntype=dna/_annot=exon

20 x95425cds_2672-3061:in_reversesequence,_3810-3857,mrna_for_ehk-1_receptor_tyrosine_kinase_

Metagene 53

k01160mrna_1077-1232,ii_histocompatibility_antigen_dc-alpha_chain_mrna_

25 m26041_1273-1405,mhc_ii_dq_alpha_mrna,_complete_cds
m63379mrna_1190-1646,trpm-2_protein_gene_u38810_2191-2659,mab-21_cell_fate-determining_protein_homolog_(cagr1)_mrna,_complete_cds_

Metagene 33

30 hg1728-ht1734_at_hg1728-ht1734_non-specific_cross_reacting_antigen,_altslice_form_2_j04046mrna_1559-2089,calmodulin_mrna,_complete_cds_s77835_88-380,_il-2=interleukin-2_[human,_brain,_mrna,_418_nt]/gb=s77835_/ntype=rna_s83362mrna_10-109,_differentiation-

35 stimulating_factor/leukemia_inhibitory_factor_receptor_{5' _region

u65581_958-1420,ribosomal_protein_l3-like_mrna,_complete_cds.

x58234mrna_31-253,mrna_for_anti-lectin_antibody_epitope_(clone_p36/8-5)

Metagene 184

d13720_3754-4319,mrna_for_lyk,_complete_cds
d30715mrna#3_3-198,_alternative_splicing;_type-2_mrna_frompap_(pancreatitis-associated_protein)_gene

5 l39061mrna_1198-1654,transcription_factor_sl1_mrna,_partial_cds_
m34276cds_2066-2228:in_reversesequence,_213-354,plasminogen_gene
u09178_3355-3898,dihydropyrimidine_dehydrogenase_mrna,_complete_cds
u37707_2429-2969 dlg3_mrna,_complete_cds_
u38291mrna_9685-10027,microtubule-associated_protein_1a_(map1a)_genomic_sequence

10 u66578cds_598-1036:in_reversesequence,_1277,putative_g_protein-coupled_receptor_(gpr23)_gene,_comple
u69263_474-1002,matrilin-2_precursor_mrna,_partial_cds_
u79667_3199-3522,alphal1a-voltage-dependent_calcium_channel_mrna,_splice_form_bi-1-v2-ggcag,_partial_

15 u87223_4830-5196,contactin_associated_protein_(caspr)_mrna,_complete_cds_
x01388cds_14-272:in_reversesequence,_349-529,mrna_for_pre-apolipoprotein_ciii_
x66358cds#1_633-1041,mrna_kkialre_for_serine/threonine_protein_kinase
x75346cds_788-1157:in_reversesequence,_1205-
1305,mrna_for_map_kinase_activated_protein_kinase_

20 Metagene 419

d13264_1681-2167,mrna_for_macrophage_scavenger_receptor_type_i,_3'_untranslated_region_
d38122_1307-1829,mrna_for_fas_ligand,_complete_cds_

25 hg1686-hg4572_s_at_hg1686-
hg4572_transcription_factor_e4tf1,_respiratory,_gammabunit,_altslice_4_
u25029_1010-1556,glucocorticoid_receptor_alpha_mrna,_variant_3'_utr
u34844exon_40-259,mercurial-insensitive_water-channel_gene,_5'_region_and_partial_exon/gb=u34844_nt

30 u52191_4854-5396,smcy_(h-y)_mrna,_complete_cds_

Metagene 331

ac002045mrna#2_625-908,_a-589h1.1_fromchromosomebac_clone_cit987-ska-
35 589h1_~complete_genomic_sequenc
d10523_3533-4079,mrna_for_2-oxoglutarate_dehydrogenase,_complete_cds_
d31840_3679-4148,drpla_mrna_for_orf,_complete_cds
d50912_2685-3183,mrna_for_kiaa0122_gene,_partial_cds_
d80008_2695-3205,mrna_for_kiaa0186_gene,_complete_cds

d86963_4563-5097,mrna_for_kiaa0208_gene,_complete_cds
 d87078_4798-5296,mrna_for_kiaa0235_gene,_partial_cds_
 hg1612-ht1612_at_hg1612-ht1612_macmarcks_
 hg2525-ht2621_at_hg2525-ht2621_helix-loop-helix_protein_delta_max,_altslice_1_
 5 hg3635-ht3845_f_at_hg3635-ht3845_zinc_finger_protein_kruppel-like_
 107648_1955-2321,mx1_mrna,_complete_cds_
 176702mrna_2447-3005,b56-delta_mrna,_complete_cds_
 m13452_1927-2435,lamin_a_mrna,_3'_end
 m91670_301-787,ubiquitin_carrier_protein_(e2-epf)_mrna,_complete_cds_
 10 s49592_1868-2425,_transcription_factor_e2f_like_protein_[human,_mrna,_2492_nt]
 u09820_5579-6058,helicase_ii_(rad54l)_mrna,_complete_cds.
 u22963_752-1238,i_histocompatibility_antigen-like_protein_mrna,_complete_cds.
 u34044_1143-1647,selenium_donor_protein_(seld)_mrna,_complete_cds
 u37012_3868-4372,cleavage_and_polyadenylation_specificity_factor_mrna,_complete_cds
 15 u52426_3469-3997,gok_(gok)_mrna,_complete_cds
 u54778_1131-1671,14-3-3_epsilon_mrna,_complete_cds_
 u57342_967-1459,myelodysplasia/myeloid_leukemia_factor(mlf2)_mrna,_complete_cds_
 u72761_2753-3233,karyopherin_beta1mrna,_complete_cds/gb=u72761/_ntype=rna
 u81984_2277-2739,endothelial_pas_domain_protein(epas1)_mrna,_complete_cds_
 20 all_x06323_1105-
 1520,mrl3_mrna_for_ribosomal_protein_l3_homologue_(mrl3=_mammalian_ribosome_l3_)_
 x71428mrna_1284-1788,fus_mrna
 x75755mrna#1_1337-1471,pr264_gene_
 all_x76717_3-268,mt-11_mrna
 25 all_x83928_456-919,mrna_for_transcription_factor_tfiid_subunit_tafii28_
 all_x90824_828-1337,mrna_for_usf2a_&_usf2b,_clone_p9dh_
 x97160mrna_2016-
 2532_tfe3_transcription_factor_gene_extracted_fromtfe3_gene,_exons_1,2,3_(and_joine
 y07595cds_948-
 30 1344:in_reversesequence,_1501,mrna_for_52_kd_subunit_of_transcription_factor_tfiih
 y13247_3077-3581,fb19_mrna
 y13620_5732-6182,mrna_for_bcl9_gene/gb=y13620/_ntype=rna
 z37166cds_1006-1252:in_reversesequence,_1432-
 1570,bat1_mrna_for_nuclear_rna_helicase_(dead_family)
 35

Metagene 295

u78551_838-1396,gallbladder_mucin_muc5b_mrna,_partial_cds_

Metagene 183

105628_4400-4969,multidrug_resistance-associated_protein_(mrp)_mrna,_complete_cds
 107541_950-1436,replication_factor_38-kda_subunit_mrna,_complete_cds
5 u28413_1440-
 1926,cockayne_syndrome_complementation_group_a_csa_protein_(csa)_mrna,_complete_cds

Metagene 20

10 af008937_508-916,syntaxin-16c_mrna,_complete_cds/gb=af008937/_ntype=rna_
 d90282_4830-5136,carbamyl_phosphate_synthetase_i_(ec_6.3.4.16)_mrna
 hg2846-ht2983_at_hg2846-ht2983_dihydrofolate_reductase,_altslice_6
 119161_1001-1385,translation_initiation_factor_eif-2_gamma_subunit_mrna,_complete_cds
 i24804_223-721,(p23)_mrna,_complete_cds
15 l36463_2081-2627,ras_inhibitor_(rin1)_mrna,_complete_cds
 l77701mrna_43-337,cox17_mrna,_complete_cds
 m90356cds_222-618:in_reversesequence_,_1194-
 1281,btf3_protein_homologue_gene,_complete_cds_
 u34301mrna_2-
20 35,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301/_ntype=dna
 u47025_3462-3994,fetal_brain_glycogen_phosphorylase_b_mrna,_complete_cds_
 u55936_367-757,snap-23_mrna,_complete_cds
 u70322_2456-3014,transportin_(trn)_mrna,_complete_cds
 x68836cds_653-1139,mrna_for_s-adenosylmethionine_synthetase
25 z18859mrna_933-
 1461,cone_transducin_alpha_subunit_gene_extracted_fromgene_for_cone_transducin_alpha_

Metagene 383

30 l11005_4386-4878,aldehyde_oxidase_(haox)_mrna,_complete_cds
 u81262_2433-2877,lerk-5_(lerk-5)_mrna,_complete_cds
 all_x89426_1465-1958,mrna_for_esm-1_protein

Metagene 339

35
 d42045_3927-4419,mrna_for_kiaa0086_gene,_complete_cds
 all_m86933_669-
 706,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds
 m96980_2034-2598,myelin_transcription_factor(mtf1)_mrna,_3'_end

all_x16282_710-1185,mrna_for_zinc_finger_protein_(clone_647)_
x89960cds_21-327:in_reversesequence,_458-698,mrna_for_mitochondrial_capsule_selenoprotein

Metagene 300

5

d15050_4757-5231,mrna_for_transcription_factor_areb6,_complete_cds_
hg3748-ht4018_at_hg3748-ht4018_basic_transcription_factor,_44_kda_subunit
s82472cds_3-
73,_beta_#name?_polymerase_beta_{exon_alpha_to_exon_vii_region}_[human,_genomic,_124_nt,

10

Metagene 291

15

af006609_5-189,rgs3_mrna,_5'_utr/gb=af006609_/ntype=rna_
d38491_298-808,mrna_for_kiaa0117_gene,_partial_cds_
d50924_3807-4083,mrna_for_kiaa0134_gene,_complete_cds
m86826_1501-2023,igf_binding_protein_complex_acid-labile_subunit_a_mrna,_complete_cds
m97252_5809-6271,kallmann_syndrome_(kal)_mrna,_complete_cds_
u27768_235-709,rgp4_mrna,_complete_cds_
u51127_1706-2084,interferon_regulatory_factor(humirf5)_mrna,_complete_cds_
u62961_2749-3241,succinyl_coa:3-oxoacid_coa_transferase_precursor_(oxct)_mrna,_complete_cds

Metagene 215

25

d67029_4839-5355,sec14l_mrna,_complete_cds_
m61916_5027-5582,laminin_b1_chain_mrna,_complete_cds_
m69225mrna_8371-8845,bullous_pemphigoid_antigen_(bpag1)_mrna,_complete_cds_
u10550_1591-2107,gem_gtpase_(gem)_mrna,_complete_cds_
u50928_4486-

30

4858,autosomal_dominant_polycystic_kidney_disease_type_ii_(pkd2)_mrna,_complete_cds
u73936_5049-5523,jagged(hj1)_mrna,_complete_cds_
u97105_4818-5364,n2a3_mrna,_complete_cds
x05908cds_814-1012:in_reversesequence,_1110-1338,mrna_for_lipocortin
all_x81895_791-1350,genx-5624_mrna,_3'_utr/gb=x81895_/ntype=rna

35

Metagene 109

hg1327-ht1327_s_at_hg1327-ht1327_statherin_
hg2723-ht2819_at_hg2723-ht2819_proto-oncogene_n-cym
hg3971-ht4241_at_hg3971-ht4241_transcription_factor

hg4332-ht4602_at_hg4332-ht4602_zinc_finger_protein_znfpt1
 107949_1619-2075,gnrh_receptor_mrna,_complete_cds_
 m11722_1473-2037,terminal_transferase_mrna,_complete_cds_
 m13143_1762-
5 2224,_nucleotide_sequence_of_the_cdna_insert_of_lambda_pk129_coding_forplasma_prekallikr
 m83363_4104-4614,plasma_membrane_calcium-pumping_atpase_(pmca4)_mrna,_complete_cds_
 s69369_779-1115,_pax3a=transcription_factor_[human,_adult_cerebellum,_mrna,_1248_nt]
 s69965_171-597,_beta-synuclein_[human,_brain,_mrna,_730_nt]
 u83117_1201-1477,sentrin_mrna,_complete_cds
10 all_x64594_1290-1855,mrna_for_50_kda erythrocyte_plasma_membrane_glycoprotein

Metagene 36

hg2538-ht2634_at_hg2538-ht2634_heterogeneous_nuclear_ribonucleoprotein_c_
15 u43653_2816-3155,obese_protein_(ob)_mrna,_complete_cds_
 v00532mrna_387-911,_ifna_gene_(interferon_alpha-
 i)_extracted_fromgene_for_leukocyte_(alpha)_interfer
 all_z46632_2953-3206,hspde4c1_gene_for_3',5'-
 cyclic_amp_phosphodiesterase,hspde4c1_gene_for_3',5'

20

Metagene 290

d13540_1948-2500,mrna_for_protein-tyrosine_phosphatase_
 s83325_1796-2275,_aspartyl(asparaginyl)beta-
25 hydroxylase_[human,_hepatoblastoma_cell_line_hepg2,_mrna
 all_x53296_1099-1657,mrna_for_irap_
 all_x95237_1357-1868,mrna_for_cysteine-rich_secretory_protein-1

Metagene 487

30

s76067cds_405-759,_cng2=cyclic_nucleotide-
 gated_cation_channel_[human,_peripheral_leucocytes,_genomi
 u13021_844-1392,positive_regulator_of_programmed_cell_death_ich-11_(ich-
 1)_mrna,_complete_cds
35 u72508_757-1105,b7_mrna,_complete_cds
 x83490exon_3-34:in_reversesequence,_389,mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(3,4))/gb=x83490/_
 z31690cds_838-1129:in_reversesequence,_1226-
 1445,(hepg2)_lal_mrna_for_lysosomal_acid_lipase_

Metagene 481

175847_1808-2330,zinc_finger_protein_45_(zmf45)_mrna,_complete_cds_
5 176465_1929-2493,nad+-dependenthydroxyprostaglandin_dehydrogenase_(pgdh)_mrna,_complete_cds_
m28585_329-839,leukocyte_interferon-alpha_mrna,_complete_cds,_clone_pifn105
u50196_1238-1760,adenosine_kinase_mrna,_complete_cds_
u92458_3747-4269,metabotropic_glutamate_receptormrna,_complete_cds

10

Metagene 355

all_x85750_1935-
2500,mrna_for_transcript_associated_with_monocyte_to_macrophage_differentiation
15 y09306cds_308-812,mrna_for_protein_kinase_dytk6,_partial/gb=y09306_ntype=rna_

Metagene 289

all_d29992_987-1132,mrna_for_placental_protein(pp5),_complete_cds_
20 m86849_1747-2179,connexin_26_(gjb2)_mrna_
all_m96132_32-66,mhc_ii_hla-dr-beta-1*09012_(hla-drb1*09012)_gene,_3'_end_cds

Metagene 236

25 m11321mrna_1193-1703,group-specific_component_vitamin_d-binding_protein_mrna,_complete_cds_
m58509cds#1_1114-1441:in_reversesequence,_4757-
4867,_fdxr_gene_(adrenodoxin_reductase)_extracted_fro
s57153_2388-
30 2878,_rbp1=retinoblastoma_binding_proteinisoform_i_{alternatively_spliced}_[_human,_mrna_
s79854_1585-
1963,_typeiodothyronine_deiodinase=selencoenzyme_[human,_placenta,_mrna,_2066_nt]_
u34360_3316-3832,lymphoid_nuclear_protein_(laf-4)_mrna,_complete_cds_
all_v01515_5300-5550,gene_encoding_preproglucagon/glucagon_is_a_29-
35 amino_acid_pancreatic_hormone_whic

Metagene 139

hg4518-ht4921_r_at_hg4518-ht4921_transcription_factor_btf3_homolog

s81083mrna_3078-3438,_<beta>-
 add_gene_extracted_from_beta_#name?_beta_subunit_63_kda_isoform/membran
 all_x86019_2045-2574,mrna_for_prpl-2_protein_

5 Metagene 72

j02986exon#3_1617-
 1983,_fgf4_gene_(transforming_protein)_extracted_fromtransforming_protein_(hst)_ge
 m22489_1036-1504,bone_morphogenetic_protein_2a_(bmp-2a)_mrna_
10 u63289_1548-2010,rna-binding_protein_cug-bp/hnab50_(nab50)_mrna,_complete_cds

Metagene 396

d14043_1834-2362,mrna_for_mgc-24,_complete_cds_
15 d26067_2680-3166,mrna_for_kiaa0033_gene,_partial_cds_
 d29805_3485-3995,mrna_for_beta-1,4-galactosyltransferase,_complete_cds_
 d29963mrna_885-1443,sfa-1_(a_member_of_transmembranesuperfamily)_mrna,_complete_cds_
 d30655_1263-1809,mrna_for_eukaryotic_initiation_factor_4aii
 d43636_3576-4080,mrna_for_kiaa0096_gene,_partial_cds_
20 d50919_3864-4404,mrna_for_kiaa0129_gene,_complete_cds
 d50926_3626-4124,mrna_for_kiaa0136_gene,_partial_cds_
 d87446_5583-6135,mrna_for_kiaa0257_gene,_partial_cds_
 d87685_5584-5920,mrna_for_kiaa0244_gene,_partial_cds_
 j04058_767-1217,electron_transfer_flavoprotein_alpha-subunit_mrna,_complete_cds
25 l14837_7335-7839,tight_junction_(zonula_occludens)_protein_zo-1_mrna,_complete_cds_
 l19872_4756-5059,ah-receptor_mrna,_complete_cds
 l40027mrna_1586-2132,glycogen_synthase_kinase_mrna,_complete_cds
 l40392mrna_1818-2280,(clone_s164)_mrna,_3'_end_of_cds_
 l48513mrna_941-1445,paraoxonase(pon2)_mrna,_complete_cds_
30 m20867_2463-2986,glutamate_dehydrogenase_(gdh)_mrna,_complete_cds
 m29204mrna#1_2236-2782,dna-binding_factor_mrna,_complete_cds_
 m31013mrna_4587-5091,nonmuscle_myosin_heavy_chain_(nmhc)_mrna,_3'_end
 m62831mrna_1210-1750,transcription_factor_etr101_mrna,_complete_cds
 m65217_1840-2278,heat_shock_factor(hsf2)_mrna,_complete_cds_
35 m77142_1629-2193,polyadenylate_binding_protein_(tia-1)_mrna,_complete_cds
 m96954_806-1313,nucleolysin_tiar_mrna,_complete_cds_
 s72008_1731-2229,_hcdc10=cdc10_homolog_[human,_fetal_lung,_mrna,_2314_nt]_
 s80562_1042-1582,_acidic_calponin_[human,_kidney,_mrna,_1607_nt]

u11313mrna_2104-2587,sterol_carrier_protein-x/sterol_carrier_protein-2_(scp-x/scp-2)_gene,_promoter_

u14588_3012-3570,paxillin_mrna,_complete_cds_

u23942_2811-3129,lanosterol_14-demethylase_cytochrome_p450_(cyp51)_mrna,_complete_cds

5 u31383_755-1151,g_protein_gamma-10_subunit_mrna,_complete_cds_

u35113_2039-2555,metastasis-associated_mta1_mrna,_complete_cds_

u43077_964-1510,cdc37_homolog_mrna,_complete_cds_

u53209_968-1436,transformer-2_alpha_(htra-2_alpha)_mrna,_complete_cds_

u61167_3488-4028,sh3_domain-containing_protein_sh3p18_mrna,_complete_cds_

10 u79267_987-1437,clone_23840_mrna,_partial_cds

u90909_944-1412,clone_23722_mrna_sequence

x04654cds_1467-1819:in_reversesequence,_2524-2634,mrna_for_u1_rna-associated_70k_protein_

all_x72727_2460-2794,tunp_mrna_for_transformation_upregulated_nuclear_protein

all_x76061_4282-4793,p130_mrna_for_130k_protein

15 x80230mrna_1187-1697,mrna_(clone_c-2k)_mrna_for_serine/threonine_protein_kinase

all_x87838_2803-3320,mrna_for_beta-catenin_

all_x98172_2240-2754,mrna_for_mach-alpha-1_protein_

all_z15115_2781-3346,top2_mrna_for_dna_topoisomerase_ii_(partial)

all_z24725_2759-3210,mitogen_inducible_gene_mig-2,_complete_cds

20

Metagene 351

d38503_915-1455,pms8_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-terminal_regio

25 hg3313-ht3490_at_hg3313-ht3490_thyroid_hormone_receptor,_beta-2

hg3996-ht4266_at_hg3996-ht4266_cpg-enriched_dna,_clone_s21_

Metagene 152

hg3115-ht3291_at_hg3115-ht3291_golli-mbp_

l02950_673-1177,mu-crystallin_mrna,_complete_cds_

all_m10950_57-304,alpha-fetoprotein_(afp)_gene

m64572_3431-3923,protein_tyrosine_phosphatase_mrna,_complete_cds_

s68134_500-665,_crem=cyclic_amp-

30 responsive_element_modulator_beta_isoform_[human,_mrna,_1030_nt]

u41898_73-505,sodium_cotransporter_rkst1_mrna,_partial_cds/gb=u41898/_ntype=rna

u50708_946-1384,branched_chain_alpha-ketoacid_dehydrogenase_e1_beta_subunit_mrna,_complete_cds_

Metagene 420

d14838_915-1317,mrna_for_fgf-9,_complete_cds_
 - d38548_4682-5210,mrna_for_kiaa0076_gene,_complete_cds
5 d63851_3157-3643,mrna_for_unc-18_homologue,_complete_cds_
 d87073_5307-5847,mrna_for_kiaa0236_gene,_complete_cds
 hg1728-ht1734_s_at_hg1728-ht1734_non-specific_cross_reacting_antigen,_altslice_form_2_
 m28827_620-1112,thymocyte_antigen_cd1c_mrna,_complete_cds
 m92449_668-1190,ltr_mrna,_3'_end_of_coding_region_and_3'_flank_
10 u02388_2097-2337,cytochrome_p450_4f2_(cyp4f2)_mrna,_complete_cds_
 u59632_2578-
 3138,h5_mrna,_partial_cds,_and_platelet_glycoprotein_ib_beta_chain_mrna,_complete_cds
 u72517_413-
 953,alternatively_spliced_variant_c7f_(c3f)_mrna,_partial_3'_utr/gb=u72517_/ntype=rna_
15

Metagene 219

d38462exon_57-
 549,gene_for_a1_chain_of_type_xix_collagen,_exon_+3'/gb=d38462_/ntype=dna/_annot=exon
20 l20433_3738-3780,octamer_binding_transcription_factor(otf1)_mrna,_complete_cds
 z68204cds_43-373,mrna_for_succinyl_coa_synthetase/gb=z68204_/ntype=rna_

Metagene 15

25 l29306_723-1116,tryptophan_hydroxylase_(tph)_mrna,_complete_cds/gb=l29306_/ntype=rna
 all_m14159_1264-1482,_t-cell_receptor_beta-chain_j2.1_gene_extracted_fromt-
 cell_receptor_germline_be
 m20566mrna_2745-3180,interleukinreceptor_mrna,_complete_cds_
 s69232_1584-1992,_electron_transfer_flavoprotein-
30 ubiquinone_oxidoreductase_[human,_fetal_liver,_mrna
 u09851_44-254,zinc_finger_protein_(znf148)_mrna,_partial_cds_
 y07512_3211-3715,mrna_for_type_i_beta_cgmp-dependent_protein_kinase_(ec_2.7.1.37)
 all_z80779_563-822,h2b/g_gene

Metagene 11

hg2662-ht2758_at_hg2662-ht2758_homeotic_protein_emx1_
 109753_1377-1827,cd30_ligand_mrna,_complete_cds_
 s71018_282-798,_cyclophilin_c_[human,_kidney,_mrna,_883_nt]_

s76473_2563-3079,_trkb_[human,_brain,_mrna,_3194_nt]

Metagene 133

- 5 all_d00726_1842-2413,mrna_for_ferrochelatase_(ec_4.99.1.1)_
d16217_1904-2414,mrna_for_calpastatin,_complete_cds
d63390_600-1164,mrna_for_acetylhydrolase_ib_beta-subunit,_complete_cds_
d87464_2481-2961,mrna_for_kiaa0274_gene,_complete_cds
hg2850-ht4814_s_at_hg2850-ht4814_biliary_glycoprotein,_altslice_5,_a
- 10 hg3578-ht3781_at_hg3578-ht3781_autoimmune_antigen,_thyroid_disease-related_antigen_
hg417-ht417_s_at_hg417-ht417_cathepsin_b_
hg4234-ht4504_at_hg4234-ht4504_methylenetetrahydrofolate_reductase_
hg4660-ht5073_at_hg4660-ht5073_microtubule-associated_protein_1b_
hg945-ht945_s_at_hg945-ht945_nucleic_acid-binding_protein
- 15 j05213_430-958,sialoprotein_mrna,_complete_cds_
l07033_967-1507,hydroxymethylglutaryl-coa_lyase_mrna,_complete_cds_
l38486mrna_1162-1720,microfibril-associated_glycoprotein(mfap4)_mrna,_3'_end_of_cds_
m71243mrna_25-
38:not_in_gb_record,glycophorin_sta_(type_a)_exonsand_4,_partial/gb=m71243_/ntype=dna_
- 20 m76424gene_6565-7070,carbonic_anhydrase_vii_(ca_vii)_gene
u01824_1402-1912,glutamate/aspartate_transporter_ii_mrna,_complete_cds_
u07000cds#4_558-810:in_reversesequence,_97660-
97876,_bcr_gene_(unknown)_extracted_frombreakpoint_clu
u13044_1429-1945,nuclear_respiratory_factor-2_subunit_alpha_mrna,_complete_cds_
- 25 u19948_1058-1616,protein_disulfide_isomerase_(pdip)_mrna,_complete_cds_
u27831cds_1110-1578:in_reversesequence,_1602-1680,striatum-
enriched_phosphatase_(step)_mrna,_partial
u44059_429-909,thyrotroph_embryonic_factor_(tef)_mrna,_complete_cds
u49441_258-
- 30 648,mitochondrial_trifunctional_protein_beta_subunit_mrna,_partial_cds/gb=u49441_/ntype=r
u51205_333-873,cop9_homolog_(hcop9)_mrna,_complete_cds_
u59057_226-754,beta-a4_crystallin_(cryba4)_mrna,_complete_cds
u59736_2496-2772,transcription_factor_(nfatc.b)_mrna,_complete_cds_
u63455mma_4412-4868,sulfonylurea_receptor_(sur1)_gene_
- 35 u67988_1623-2163,guanylate_kinase_associated_protein_(gkap)_mrna,_complete_cds_
u86358_296-818,chemokine_(teck)_mrna,_complete_cds/gb=u86358_/ntype=rna
u90918_1794-2094,clone_23654_mrna_sequence_
u96769mrna_1266-1746,chondroadherin_gene,_5'_flanking_region_and_

u96781mrna#1_2433-2961,_atp2a1_gene_(ca2+_atpase_of_fast-twitch_skeletal_muscle_sacoplasmic_reticul
 x65633cds_585-870:in_reversesequence,_1568-1766,acth-r_gene_for_adrenocorticotrophic_hormone_receptor
5 x66114mrna_564-1074,gene_for_2-oxoglutarate_carrier_protein_all_x77197_2631-3166,mrna_for_chloride_channel_x83973cds_2262-2538:in_reversesequence,_2738-2822,mrna_for_ttf-i
 x91117mrna_1655-2033,hg_net_gene_exon_1_x92521cds_1127-1484:in_reversesequence,_1618-1768,mrna_for_mmp-19_protein
10 x93996mrna_2570-3113,mrna_for_afx_protein_x95406exon#1-2_12-17:not_in_gb_record,cyclin_e_gene.
 y07847exon#3_36-582,mrna_for_rrp22_protein_z71389mrna_85-295,mrna_for_skin-antimicrobial-peptide(sap1).

15 Metagene 61

m31166mrna_1286-1784,tumor_necrosis_factor-inducible_(tsg-14)_mrna,_complete_cds_u60415_2126-2570,bhlh-pas_protein_jap3_mrna,_complete_cds_u70981_749-1283,interleukin-13_receptor_mrna,_complete_cds
20 z83803_7-259,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc4)

Metagene 463

hg2709-ht2805_at_hg2709-ht2805_serine/threonine_kinase
25 hg3137-ht3313_at_hg3137-ht3313_zinc_finger_protein_znf81_hg4052-ht4322_at_hg4052-ht4322_glutamate_ionotropic_receptor
 m13666_800-992,c-myb_mrna,_3'_end_m15656cds_712-1066:in_reversesequence,_3992-4082,aldolase_b_(aldob)_gene_m54995_108-603,connective_tissue_activation_peptide_iii_mrna,_complete_cds
30 s69790_962-1412,_brush-1=tumor_suppressor_{3'_region}_[human,_breast_epithelium,_mrna_partial,_1485_all_x53065_85-462,spr2-1_gene_for_small_proline_rich_protein_(exon_2)
 y10571cds_696-978:in_reversesequence,_1002-1194,mrna_for_ding_gene_all_y11897_19-320,brx_gene_3'_utr/gb=y11897_/ntype=rna
35 z75330cds_3384-3714:in_reversesequence,_4156-4312,mrna_for_nuclear_protein_sa-1.

Metagene 414

d86640_2374-2902,mrna_for_stac,_complete_cds

hg2157-ht2227_at_hg2157-ht2227_mucin_4,_tracheobronchial_
 j03507_3421-3865,complement_protein_component_c7_mrna,_complete_cds
 all_115296_3031-3082,clone_hrcnc2b_retinal_rod_cyclic_nucleotide-
 gated_cation_channel_gene,_complete
5 141390exon#1_244-395,corebeta-1,6-n-
 acetylglucosaminyltransferase_(coregnt)_gene,_exon/gb=141390_/nt
 m59820mrna_2435-2975,granulocyte_colony-
 stimulating_factor_receptor_(csf3r)_mrna,_complete_cds_
 m77481mrna_1021-1566,antigen_(mage-1)_gene,_complete_cds
10 m82962mrna_2313-2835,n-benzoyl-l-tyrosyl-p-amino-
 benzoic_acid_hydrolase_alpha_subunit_(pph_alpha)_mr
 m87284_2479-2923,69_kda_2'_S'_oligoadenylate_synthetase_(p69_2-
 5a_synthetase)_mrna,_complete_cds_
 u05291_1363-1849,fibromodulin_mrna,_partial_cds
15 u29589exon_2948-3488,m3_muscarinic_acetylcholine_receptor_(chrn3)_gene,_complete_cds_
 u43672_2939-3443,putative_transmembrane_receptor_il-1rrp_mrna,_complete_cds
 u71601_960-1422,zinc_finger_protein_zfp47_(zf47)_mrna,_partial_cds_
 x06482cds_60-405:in_reversesequence,_884-887,theta_1-globin_gene
 all_x14975_7566-8337,cd1_r2_gene_for_mhc-related_antigen_
20 x55989mrna_169-354,ecrp_gene_for_eosinophil_cationic_related_protein
 y10512mrna_14-452,mrna_for_cd282_protein/gb=y10512_/ntype=rna

Metagene 113

25 l10102mrna#1_392-794,sex-determining_region_y_(sry)_gene,_complete_cds_
 l34081mrna_1055-1601,bile_acid_coa:_amino_acid_n-acyltransferase_mrna,_complete_cds
 m34353_6763-7342,transmembrane_tyrosine-specific_protein_kinase_(ros1)_mrna,_complete_cds
 m61156_1122-1308,activator_protein_2b_(ap-2b)_mrna,_complete_cds_
 m95767_1065-1563,di-n-acetylchitobiase_mrna,_complete_cds_
30 all_x02956_1039-1253,interferon_alpha_gene_ifn-alpha_5_
 all_x07994_5703-6244,mrna_for_lactase-phlorizin_hydrolase_lph_(ec_3.2.1.23-62)_
 x68994exon_4-55,creb_gene,_exon_y
 all_x78686_706-1121,ena-78_mrna
 all_x95239_863-1362,mrna_for_cysteine-rich_secretory_protein-2/type_i
35 y10508mrna_370-660,mrna_for_cd190_protein/gb=y10508_/ntype=rna_

Metagene 106

hg2007-ht2056_s_at_hg2007-ht2056_proto-oncogene_sno,_altslice_n_

Metagene 319

d42072_2020-2542,mrna_for_nfl_n-isoform-exon11,_complete_cds_

5 hg3998-ht4268_at_hg3998-ht4268_l-glycerol-3-phosphate:nad+_oxidoreductase
m28170_1894-1987,cell_surface_protein_cd19_(cd19)_gene,_complete_cds_
m62843_906-
1404,brain_protein_recognized_by_the_sera_of_patients_with_paraneoplastic_sensory_neurono
s67247_365-

10 821,_smooth_muscle_myosin_heavy_chain_isoform_smemb_[human,_umbilical_cord,_fetal_aorta,_
u08006exon#1_78-567,complementalpha_subunit_(c8a)_gene
u09411_1794-2343,zinc_finger_protein_znf132_mrna,_complete_cds_
u40343_657-1119,cdk_inhibitor_p19ink4d_mrna,_complete_cds
u52827_1022-1508,cri-du-chat_region_mrna,_clone_nibb11_-

15 u66052mrna_7-271,clone_w2-6_mrna_from_chromosome_x/gb=u66052_/ntype=rna
x07173cds_2503-2803:in_reversesequence_,2956-3028,mrna_for_second_protein_of_inter-alpha-
trypsin_inh
x16316cds_2109-2355:in_reversesequence_,2483-2693,mrna_for_vav_oncogene_
x63578mrna_31-535,gene_for_parvalbumin

20

Metagene 170

109230_933-1460,c-c_chemokine_receptor_type(c-c_ckr-1)_mrna,_complete_cds_

147276_383-934,(cell_line_hl-60)_alpha_topoisomerase_truncated-
25 form_mrna,_3'_utr/gb=147276_/ntype=rn
m13150mrna_776-1337,mas_proto-oncogene_mrna,_complete_cds
m20137mrna_400-820,interleukin(il-3)_mrna,_complete_cds,_clone_pcd-sr-alpha_-
u33202_104-354,mdm2-d_(mdm2)_mrna,_complete_cds/gb=u33202_/ntype=rna_-
all_x66894_3881-4417,facc_mrna_from_complementation_group_c_(fa(c))

30 all_y08263_1373-1902,mrna_for_aad14_protein,_partial_-
all_y09980_16580-17121,hoxd3_gene_-

Metagene 75

35 hg1227-ht1227_s_at_hg1227-ht1227_collagen_type_ii_alpha_1
all_j00116_4597-4806,alpha-1(ii)_collagen_gene_col2a1,_partial_cds_
m60299exon_73-163,alpha-
1_collagen_type_ii_gene,_exons_1, and/gb=m60299_/ntype=dna/_annot=exon
u14550_1319-1877,sialyltransferase_sthm_(sthm)_mrna,_complete_cds

u22322_2205-2587,nuclear_tyrosine_protein_kinase_rak_mrna,_complete_cds
 all_x57830_2409-3016,serotonin_5-ht2_receptor_mrna_

Metagene 223

5

all_m60749_829-1061,histone_h4_(h4)_gene,_complete_cds_
 u24577_1182-1512,ldl-phospholipase_a2_mrna,_complete_cds_

Metagene 116

10

d63412_1299-1713,mrna_for_aquaporin,_complete_cds
 hg2981-ht3938_s_at_hg2981-ht3938_epican,_altslice_12
 u61849_4650-5040,neuronal_pentraxin(nptx1)_mrna,_complete_cds_

15 Metagene 332

137362_1009-1579,(clone_d2-115)_kappa opioid_receptor_(oprk1)_mrna,_complete_cds
 all_m28879_3325-4444,granzyme_b_(ctla-1)_gene,_complete_cds
 u34070cds_744-1053:in_reversesequence,_1731-
20 1763,ccaaat/enhancer_binding_protein_alpha_gene,_complete
 u57592_3563-4043,jumonji_putative_protein_(jumonji)_mrna,_complete_cds_
 u93867_1248-
 1764,rna_polymerase_iii_subunit_(rpc62)_mrna,_complete_cds/gb=u93867_/ntype=rna
 all_z28339_2084-2649,mrna_for_delta_4-3-oxosteroidbeta-reductase

25

Metagene 196

d37984_1856-2314,mrna_for_dna_helicase_q1,_partial_cds_
 122214_2335-2857,adenosine_a1_receptor_(adora1)_mrna_exons_1-6,_complete_cds_
30 u17743_699-1221,jnk_activating_kinase_(jnk1)_mrna,_complete_cds_
 u21051mrna#1_2326-2647,g_protein-coupled_receptor_(gpr4)_gene,_complete_cds_
 u45975_882-1434,phosphatidylinositol_(4,5)bisphosphate_5-
 phosphatase_homolog_mrna,_partial_cds_
 u50743_13-439,na,k-atpase_gamma_subunit_mrna,_complete_cds_

35

Metagene 150

d17390_2313-2829,mrna_for_mdc_protein
 d49410exon_48-534,gene_for_interleukinreceptor_alpha_subunit

hg3063-ht3224_at_hg3063-ht3224_major_histocompatibility_complex_i
 hg3355-ht3532_at_hg3355-ht3532_peroxisome_proliferator_activated_receptor
 hg4417-ht4687_f_at_hg4417-ht4687_homeotic_protein_hpx-2
 111931_1454-1644, cytosolic_serine_hydroxymethyltransferase_(shmt)_mrna,_complete_cds_
5 m21056cds_193-403:in_reversesequence,_165-345,pancreatic_phospholipase_a-2_(pla-2)_gene_
 m76231_292-790, sepiapterin_reductase_mrna,_complete_cds
 m81379_1126-1546, alpha-3_type_iv_collagen_(col4a3)_mrna,_3'_end
 m86383_1007-1527, nicotinic_acetylcholine_receptor_alpha_subunit_mrna,_complete_cds_
 m86407_2299-2833, alpha_actinin(actn3)_mrna,_complete_cds_
10 m95678_3990-4494, phospholipase_c-beta-2_mrna,_complete_cds
 u06643_71-463, keratinocyte_lectin(hkl-14)_mrna,_complete_cds.
 u16127_3025-3589, glutamate/kainate_receptor_subunit_(eaa5)_mrna,_complete_cds
 u43142_1456-1972, vascular_endothelial_growth_factor_related_protein_vrp_mrna,_complete_cds_
 u59913_1640-2168, chromosomemad_homolog_smad5_mrna,_complete_cds_
15 u62437_1943-2393, nicotinic_acetylcholine_receptor_beta2_subunit_precursor,_mrna,_complete_cds
 u71300_1307-
 1703, snrRNA_activating_protein_complex_50kd_subunit_(snap50)_mrna,_complete_cds_
 all_x15217_2292-2875, sno_oncogene_mrna_for_snoa_protein_ski-related_
 all_x54741_2389-2918, cypxib2_gene_for_aldosterone_synthase_
20 x60592mrna_415-973, cdw40_mrna_for_nerve_growth_factor_receptor-related_b-
 lymphocyte_activation_molec
 x60655mrna_990-1474, evx1_mrna
 x62891mrna_57-390, mutant_coseg_gene_for Vasopressin-neurophysin_precursor
 x91257_1281-1797, mrna_for_seryl-tRNA_synthetase
25 x92475_905-1295, mrna_for_itba1_protein_
 x95191cds_707-848, mrna_for_delta-sarcoglycan/gb=x95191/_ntype=rna
 all_y11215_971-1446, mrna_for_skap55_protein/gb=y11215/_ntype=rna
 z22865cds_164-578:in_reversesequence,_620, dermatopontin_mrna,_complete_cds
 reverse_z49155_27087-
30 27346, dna_from_cosmid_183d3, huntington's_disease_region,_chromosome_4p16.3_

Metagene 263

ab003698_2634-3138, mrna_for_cdc7-related_kinase,_complete_cds
35 m77140_91-409, pro-galanin_mrna,_3'_end_
 m98447mrna_2256-2670, keratinocyte_transglutaminase_gene,_complete_cds_
 u23752_1679-1919, sox-11_mrna,_complete_cds

Metagene 282

aj001421cds_117-567:in_reversesequence,_585-
 600,mrna_for_rer1_protein/gb=aj001421_ntype=rna_
 d86981_5936-6410,mrna_for_kiaa0228_gene,_partial_cds_

5 142452mrna_1100-1520,pyruvate_dehydrogenase_kinase_isoenzyme(pdk3)_mrna,_complete_cds
 m22632mrna_1744-2284,mitochondrial_aspartate_aminotransferase_mrna,_complete_cds_
 m87503_1085-1535,ifm-responsive_transcription_factor_subunit_mrna,_complete_cds
 u01923_1649-2090,btk_region_clone_ftp-3_mrna_
 u02081_1642-2026,guanine_nucleotide_regulatory_protein_(net1)_mrna,_complete_cds_

10 u04285utr#1_689-1148,lysosomal_acid_lipase,_cholesteryl_estер_hydrolase_(lipa)_gene
 u16799_865-1419,na,k-atpase_beta-1_subunit_mrna,_complete_cds
 u40038_1236-1425,gtp-binding_protein_alpha_q_subunit_(gnaq)_mrna,_complete_cds_
 u53445_2442-
 2928,ovarian_cancer_downregulated_myosin_heavy_chain_homolog_(doc1)_mrna,_complete_cds_

15 u58046_4637-5176,p167_mrna,_complete_cds_
 u76421_4572-4962,dsrna_adenosine_deaminase_drada2b_(drada2b)_mrna,_complete_cds
 u77718_2100-2592,desmosome_associated_protein_pinin_mrna,_complete_cds_
 u81006_1886-2348,p76_mrna,_complete_cds
 u89505_1087-1537,hlark_mrna,_complete_cds

20 u94586_145-445,nadh:ubiquinone_oxidoreductase_mlrq_subunit_mrna,_complete_cds
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 all_x13916_14416-14876,mrna_for_ldl-receptor_related_protein_
 x53586mrna_4766-
 5306,_integrin_alpha(or_alpha_e)_protein_gene_extracted_frommrna_for_integrin_alpha_

25 all_x68560_2909-3480,spr-2_mrna_for_gt_box_binding_protein_
 x69978cds_3218-3494:in_reversesequence,_3769-3781,mrna_for_xp-g_factor
 all_x71490_1059-1552,mrna_for_vacuolar_proton_atpase,_subunit_d
 all_x72790_30-1461,endogenous_retrovirus_mrna_for_orf/gb=x72790_ntype=rna_
 x77909cds_888-1122:in_reversesequence,_1202-1406,ikbl_mrna

30 x82676_3333-3873,mrna_for_tyrosine_phosphatase_
 all_y00757_629-1134,mrna_for_polypeptide_7b2_
 all_z34975_2303-2862,ldlc_mrna_
 z49989cds_779-1079:in_reversesequence,_1540,mrna_for_smoothelin_

35 Metagene 85

d38553_2125-2665,mrna_for_kiaa0074_gene,_partial_cds_
 d78367_1372-1810,mrna_for_k12_keratin,_complete_cds
 j03133_2096-2612,transcription_factor_sp1_mrna,_3'_end_

106895_503-977,antagonizer_of_myc_transcriptional_activity_(mad)_mrna,_complete_cds_
 141816mrna_891-1389,cam_kinase_i_mrna,_complete_cds_
 s78085_719-1187,_pdcd2=programmed_cell_death-
 2/rp8_homolog_[human,_fetal_lung,_mrna,_1282_nt]_

5 all_u66083_2217-
 2758,contig_of_two_cosmids_from_llnl_x_chromosome_library_(u83f1,_u109h10),_includin
 u89916_375-879,putative_osp_like_protein_mrna,_partial_cds
 all_x62048_1820-2343,wee1_hu_gene

10 Metagene 385

m32402mrna_1851-2253,placental_protein_(pp11)_mrna,_complete_cds_
 m93107_978-1278,heart_(r)-3-hydroxybutyrate_dehydrogenase_mrna,_3'_end

15 Metagene 465

af015913_1437-1947,skb1hs_mrna,_complete_cds/gb=af015913_/ntype=rna_
 d11428_1253-1757,mrna_for_pmp-22(pas-ii/sr13/gas-3)_of_peripheral_myelin,_complete_cds_
 d16294_1019-1523,mrna_for_mitochondrial_3-oxoacyl-coa_thiolase,_complete_cds_

20 d21063_2853-3303,mrna_for_kiaa0030_gene,_partial_cds_
 d38524_2673-3213,mrna_for_5'_-nucleotidase_
 d63476_4587-4953,mrna_for_kiaa0142_gene,_complete_cds
 hg1827-ht1856_s_at_hg1827-ht1856_cytochrome_p450,_subfamily_iic,_altslice_form_2
 hg2981-ht3127_s_at_hg2981-ht3127_epican,_altslice_11

25 hg3521-ht3715_at_hg3521-ht3715_ras-related_protein_rap1b_
 j05682_1023-1575,subunit_c_of_v-atpase_(vat_c)_mrna,_3'_end
 l28997_443-953,arl1_mrna,_complete_cds
 l31801_2229-2535,monocarboxylate_transporter(slcl6a1)_mrna,_complete_cds_
 m25753mrna_1103-1427,cyclin_b_mrna,_3'_end_

30 all_m27161_6940-7265,mhc_i_cd8_alpha-chain_(leu-2/t8)_gene,_complete_cds_
 m67468_3244-3720,fragile_x_mental_retardationfinr-1_gene,_3'_end,_clones_bc72_and_bc22_
 m74524_1190-1658,hhr6a_(yeast_radhomologue)_mrna,_complete_cds
 m90656_2044-2590,gamma-glutamylcysteine_synthetase_(gcs)_mrna,_complete_cds
 u00001_2019-2547,homologue_of_spombe_nuc2+_and_anidulans_bima

35 u01833_690-1164,nucleotide-binding_protein_mrna,_complete_cds
 u09564_3725-4205,serine_kinase_mrna,_complete_cds
 u15128cds_1011-1299:in_reversesequence,_2065-2233,beta-1,2-n-
 acetylglucosaminyltransferase_ii_(mgat2)
 u17714_2774-3068:not_in_gb_record,putative_tumor_suppressor_(snc6)_mrna,_complete_cds_

u27460_1582-1798,uridine_diphosphoglucose_pyrophosphorylase_mrna,_complete_cds_
 u39318_159-675,e2_ubiquitin_conjugating_enzyme_ubch5c_(ubch5c)_mrna,_complete_cds
 u61145_2035-2509,enhancer_of_zeste_homolog(ezh2)_mrna,_complete_cds_
 u61232_1407-1869,tubulin-folding_cofactor_e_mrna,_complete_cds_
5 u69141_1311-1719,glutaryl-coa_dehydrogenase_mrna,_complete_cds_
 u72263_2410-
 2931,multiple_exostoses_type_ii_protein_ext2.i_mrna,_complete_cds/gb=u72263_ntype=rna_
 u88047_1567-1969,dna_binding_protein_homolog_(drx)_mrna,_partial_cds_
 all_x02160_4717-4976,mrna_for_insulin_receptor_precursor_
10 all_x54993_1096-1685,tfiid_mrna
 all_x56807_2617-3194,dsc2_mrna_for_desmocollins_type_2a_and_2b_
 x59244mrna_2391-2967,znf43_mrna
 x61100mrna_1983-
 2445,_75_kda_subunit_nadh_dehydrogenase_precursor_gene_extracted_frommrna_for_mitoch
15 all_x63468_2398-2915,mrna_for_transcription_factor_tfiie_alpha_
 all_x64229_888-1393,dek_mrna_
 x65867cds#1_1157-1409:in_reversesequence,_1447-1639,mrna_for_adenylosuccinate_lyase_
 all_x79201_2342-2775,mrna_for_syt
 x85753_1268-1646,mrna_for_cdk8_protein_kinase
20 y00971mrna_1891-
 2419,mrna_for_phosphoriobosyl_pyrophosphate_synthetase_subunit_ii_(ec_2.7.6.1)_
 y09943cds_117-452:in_reversesequence,_561-602,mrna_for_ngf-inducible_pc3_antiproliferative_protein_
25 Metagene 411

d17570_565-1083,mrna_for_zona-pellucida-binding_protein_(sp38),_complete_cds.
 d49394_1619-2123,mrna_for_serotonin_5-ht3_receptor,_complete_cds_
 hg2358-ht4858_s_at_hg2358-ht4858_proto-oncogene_ets-1,_altslice_2_

30 l39833_2587-3097,(clone_hkvbeta3)_k+_channel_beta_subunit_mrna,_complete_cds
 m13577mrna_1550-2096,myelin_basic_protein_(mbp)_mrna,_complete_cds_
 m14113mrna_8440-8986,coagulation_factor_viii:c_mrna,_complete_cds
 all_m33987_2226-2701,carbonic_anhydrase_i_(ca1)_mrna,_complete_cds_
 m35296_3284-3758,tyrosine_kinase_arg_gene_mrna_

35 m64934_1917-2397,kell_blood_group_protein_mrna_
 all_s71129_3-426,_acetylcholinesterase_{i4-
 e5_domain}_{[human,tumor_cell_lines,genomic,847_nt]}
 s78234_2755-3259,_nuc2_homolog_[human,fibroblasts,mrna,3320_nt]
 u00238_3024-3552,glutamine_prpp_amidotransferase_(gpat)_mrna_complete_cds

u00943_1017-1203,clone_a9a2brb2_(cac)n/(gtg)n_repeat-containing_mrna_
 u03397_787-1358,receptor_protein_4-1bb_mrna,_complete_cds
 u15460_322-844,bzip_protein_b-atf_mrna,_complete_cds_
 u27326_1666-
5 2123,alpha_(1,3/1,4)_fucosyltransferase_(fut3)_mrna,_major_transcript_i,_complete_cds
 u31875_979-1399,hep27_protein_mrna,_complete_cds.
 u40846_1964-2399,alpha-n-acetylglucosaminidase_(nag)_mrna,_complete_cds
 u51477_2883-3444,diacylglycerol_kinase_zeta_mrna,_complete_cds_
 u62317mrna#6_1634-
10 2156,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
 u71364_1097-1553,serine_proteinase_inhibitor_(p19)_mrna,_complete_cds
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 35099,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted_from
 u79274_883-1381,clone_23733_mrna,_complete_cds.
15 v00574cds_225-538:in_reversesequence,_3330-
 3468,germ_line_gene_homologous_to_bladder_carcinoma_oncog
 all_x17622_3693-4210,hbk2_mrna_for_potassium_channel_protein_
 x51688mrna_1054-1438,mrna_for_cyclin_a_
 all_x62515_13260-13708,mrna_for_basement_membrane_heparan_sulfate_proteoglycan_
20 x70040cds_3944-4130:in_reversesequence,_4236-4470,ron_mrna_for_tyrosine_kinase_
 x85781exon_2-551,nos2_gene,_exon_27/_gb=x85781/_ntype=dna/_annot=exon
 y10055cds_2802-3096:in_reversesequence,_3310-3532,mrna_for_phosphoinositide_3-kinase_

Metagene 326

25

l10035_162-666:in_reversesequence,_684-690,crystallin_beta-b2_mrna,_complete_cds
 m16594_790-904,glutathione_s-transferase_ha_subunit(gst)_mrna,_complete_cds_
 u81523_1378-1870,endometrial_bleeding_associated_factor_mrna,_complete_cds.
 all_y10375_1179-1706,mrna_for_sirp-alpha1

30

Metagene 237

d17427_3421-3506,mrna_for_desmocollin_type_4_
 d25278_2024-2510,mrna_for_kiaa0036_gene,_complete_cds
35 d26528_1017-1515,mrna_for_rna_helicase,_complete_cds_
 d32202_2017-2263,mrna_for_alpha_1c_adrenergic_receptor_isoform_2,_complete_cds_
 d43768_663-1197,_numan_mrna_for_scm-1_(single_cysteine_motif-1),_complete_cds_
 all_d49742_2413-2984,mrna_for_hgf_activator_like_protein,_complete_cds_

d49817_1233-1725,mrna_for_fructose_6-phosphate,2-kinase/fructose_2,6-bisphosphatase,_complete_cds

d49950_495-918,liver_mrna_for_interferon-gamma inducing_factor(igif),_complete_cds_d64158_415-

5 668:not_in_gb_record,mrna_for_atp_binding_protein_associated_with_cell_differentiation,_p d82061_357-876,b-cell_mrna_for_a_member_of_the_short-chain_alcohol_dehydrogenase_family,_partial_cds

d82343_474-960,mrna_for_amy,_complete_cds

d88270exon#2_89-293:in_reversesequence,_18899-

10 19103,(lambda)_dna_for_immunoglobulin_light_chain
 hg1804-ht1829_at_hg1804-ht1829_ornithine_aminotransferase-like
 hg2367-ht2463_s_at_hg2367-ht2463_trithorax_homolog_hrx_
 hg2416-ht2512_at_hg2416-ht2512_gal_beta_1,3(4)glcnac_alpha2,3-sialyltransferase
 hg2562-ht2658_s_at_hg2562-ht2658_a-myb_

15 hg2689-ht2785_at_hg2689-ht2785_mucin_5b,_tracheobronchial
 hg3364-ht3541_at_hg3364-ht3541_ribosomal_protein_l37_
 hg4102-ht4372_at_hg4102-ht4372_n-ethylmaleimide-sensitive_factor_
 hg4115-ht4385_at_hg4115-ht4385_olfactory_receptor_or17-210_
 hg4333-ht4603_at_hg4333-ht4603_zinc_finger_protein_znfpt7

20 hg961-ht961_at_hg961-ht961_guanine_nucleotide_exchange_factor_
 j00073exon#2_132-255:not_in_gb_record,alpha-cardiac_actin_gene,_5'_flank_and
 j00306cds_40-304:in_reversesequence,_1168-2537,somatostatin_i_gene_and_flanks_
 l40371mrna_661-1075,thyroid_receptor_interactor_(trip4)_mrna,_3'_end_of_cds_
 l42354mrna_25-409,(clone_48es4)_mrna_fragment/gb=142354/_ntype=rna

25 l42451mrna_947-1397,pyruvate_dehydrogenase_kinase_isoenzyme(pdk2)_mrna,_complete_cds_
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 m12963mrna_871-985,i_alcohol_dehydrogenase_(adh1)_alpha_subunit_mrna,_complete_cds_
 m14091mrna_1209-1731,thyroxine-binding_globulin_mrna,_complete_cds_
 m14123cds#2_830-1280,_pol_fromendogenous_retrovirus_herv-

30 k10/gb=m14123/_ntype=dna/_annot=cds,_pol_fr
 m14123cds#3_13-175,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123/_ntype=dna/_annot=cds,_pol_from
 m25629_270-846,kallikrein_mrna,_complete_cds,_clone_clone_phkk25_
 m25809_1358-1817,endomembrane_proton_pump_subunit_mrna,_complete_cds_

35 m26958_46-235,parathyroid_hormone-related_protein_(pthrP)_mrna,_5'_flank,_clone_pbrf52/gb=m26958/_nt
 m29194cds_1090-1408:in_reversesequence,_175-223,triglyceride_lipase_gene
 m29994exon#1_2-80,alpha-i_spectrin_gene,_exon/gb=m29994/_ntype=dna/_annot=exon_
 m31241_s_at_m31241_m31241,not_in_gb_record,complement_receptor(cr1)_gene_

m60721mrna_1630-2182,homeobox_gene,_complete_cds_
m62982_1795-2299,arachidonate_12-lipoxygenase_mrna,_complete_cds_
m63603_1052-1574,phospholamban_mrna,_complete_cds
m63928_645-1161,t_cell_activation_antigen_(cd27)_mrna,_complete_cds_

5 m74093_1283-1685,cyclin_mrna_
m83664_1098-1416,mhc_ii_lymphocyte_antigen_(hla-dp)_beta_chain_mrna,_complete_cds
m89914_8414-8952,neurofibromin_(nfl)_gene,_complete_cds
m93283_898-1438,pancreatic_lipase_related_protein(plrp1)_mrna,_complete_cds_
m99438_1768-2332,transducin-like_enhancer_protein_(tle3)_mrna,_complete_cds

10 s69115_250-808,_granulocyte_colony-stimulating_factor_induced_gene_[human,_cml_patient,_bone_marrow,_
s76756_510-954,_4r-map2=microtubule-associated_protein4r_isoform_[human,_brain,_mrna_partial,_1012_n
u00944_1121-1619,clone_a9a2brb6_(cac)n/(gtg)n_repeat-containing_mrna_

15 u04806_247-787,flt3/flk2_ligand_mrna,_complete_cds.
u09367_1942-2449,zinc_finger_protein_znf136
u20230exon_7-127,guanyl_cyclase_c_gene,_partial_cds/gb=u20230/_ntype=dna/_annot=exon_
u23430exon_172-496:in_reversesequence,_793-994,cholecystokinin_type_a_receptor_(cck-a)_gene
u33052_2643-3212,lipid-activated,_protein_kinase_prk2_mrna,_complete_cds_

20 u34038_880-1390,proteinase-activated_receptor-2_mrna,_complete_cds_
u37143_1256-1832,cytochrome_p450_monomooxygenase_cyp2j2_mrna,_complete_cds_
all_u37219_2132-2583,cyclophilin-like_protein_cyp-60_mrna,_complete_cds
u40223cds_660-
1068:in_reversesequence,_1548,uridine_nucleotide_receptor_(unr)_gene,_complete_cds

25 u47011mrna#1_581-791:in_reversesequence,_751-
961,_fgf8_gene_(fibroblast_growth_factorprecursor)_extr
u48707_123-597,protein_phosphatase-1_inhibitor_mrna,_complete_cds
u50527_1493-1891,brca2_region,_mrna_sequence_cg018_
u59286_49-439,beta-r1_mrna,_partial_cds/gb=u59286/_ntype=rna_

30 u59321_1625-1967,dead_box_protein_p72_(p72)_mrna,_complete_cds_
u60519_2965-3499,apoptotic_cysteine_protease_mch4_(mch4)_mrna,_complete_cds
u66048mrna_2400-2838,clone_161455-2-3_b_cell_expressed_mrna_from_chromosome_x
u66088_1895-2369,sodium_iodide_symporter_mrna,_complete_cds
u71088_1325-1586,map_kinase_kinase_mek5c_mrna,_complete_cds

35 u75272_743-1283,gastricsin_mrna,_complete_cds
u75276_2760-3225,tfiib_related_factor_hbrf_(hbrf)_mrna,_complete_cds.
u79115_337-886,death_adaptor_molecule_raidd_(raidd)_mrna,_complete_cds.
u79253_734-1100,clone_23893_mrna,_complete_cds.

u90306_13-175,iroquois-class_homeodomain_protein_irx-
 4_mrna_partial_cds/gb=u90306_ntype=rna
 u96629mrna#1_1142-
 1658,_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_clon
5 all_x00588_5021-5514,mrna_for_precursor_of_epidermal_growth_factor_receptor
 x02612mrna#3_656-1184,gene_for_cytochrome_p(1)-450_
 all_x03663_3391-3824,mrna_for_c-fms_proto-oncogene_
 x17254cds_911-1211:in_reversesequence,_1335-1449,mrna_for_the_transcription_factor_eryf1
 x54673cds_1493-1775:in_reversesequence,_2015-2135,gat1_mrna_for_gaba_transporter
10 all_x65873_3040-3551,mrna_for_kinesin_(heavy_chain)
 x65977cds_118-268:in_reversesequence,_325-499,mrna_for_corticostatin_hp-4_precursor_
 all_x74301_4170-4479,mrna_for_mhc_ii_transactivator
 all_x78416_369-921,alpha-s1-casein_mrna
 all_x80878_4120-4349,r_kappa_b_mrna
15 all_x82895_2890-3425,mrna_for_dlg2_
 x95190cds_1574-1958:in_reversesequence,_2170,mrna_for_branched_chain_acyl-coa_oxidase_
 x97302mrna_40-235,mrna_for_ptg-1_protein/gb=x97302_ntype=rna
 x99393cds_292-552:in_reversesequence,_655-787,cmkbr5_gene,_non-functional_mutant
 y11999cds_31-358,mrna_for_inositol_1,4,5-trisphosphate_3-kinase/gb=y11999_ntype=rna_
20 z29090cds_2967-3183:in_reversesequence,_3201-3393,mrna_for_phosphatidylinositol_3-kinase
 z69923cds_1572-1818:in_reversesequence,_6905-
 7019,dna_sequence_from_cosmid_1219f9,_huntington's_dise
 z84483cds_1166-1676,dna_sequence_from_pac_46h23,_brca2_gene_region_chromosome_13q12-
 13_contains_klot
25
 Metagene 218

 d89377_1587-2148,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
 101042_2723-3209,hiv1_tata_element_modulatory_factor_mrna_sequence_from_chromosome_3_
30 102932_1331-1829,peroxisome_proliferator_activated_receptor_mrna,_complete_cds_
 140636_3438-3822,(clone_fbk_iii_16)_protein_tyrosine_kinase_(net_ptk)_mrna,_complete_cds
 177571mrna_1738-2218,dgs-a_mrna,_3'_end_
 m13207exon#2-4_6-288:in_reversesequence,_2583:not_in_gb_record,granulocyte-
 macrophage_colony-stimula
35 all_m19159_3664-4193,placental_heat-stable_alkaline_phosphatase_(plap-1)_gene,_complete_cds
 m20681mrna#2_3326-3842,glucose_transporter-like_protein-iii_(glut3),_complete_cds
 m21934_at_m21934_m21934,not_in_gb_record,rearranged_and_truncated_ig_gamma_heavy_chain
 disease(riv)

m22005cds_49-367,interleukingene,_clone_pattacil-2c/2tt,_complete_cds,_clone_pattacil-
2c/2tt/gb=m220

m28210_356-686,gtp-binding_protein_(rab3a)_mrna,_complete_cds_

m30894_1015-1513,t-cell_receptor_ti_rearranged_gamma-chain_mrna_v-j-c_region,_complete_cds_

5 m62800mma_1350-1827,52-kd_ss-a/ro_autoantigen_mrna,_complete_cds

u28833_1571-2075,down_syndrome_critical_region_protein_(dscr1)_mrna,_complete_cds

u47292exon_120-564,spasmolytic_polypeptide_(sp)_gene,_5'_region_and

u64675_1439-1853,sperm_membrane_protein_bs-63_mrna,_complete_cds_

u66838_1138-1594,cyclin_a1_mrna,_complete_cds

10 u67614_at_u67614_u67614,not_in_gb_record,sinusoidal_reduced_glutathione_transporter-
associated_prote

all_x54457_2328-2416,mrna_for_bile-salt-stimulated_lipase_(bssl)_(_ec_3.1.1.3)

all_x59656_1286-1827,crk-like_gene_crkl

all_x76342_1484-2019,adh7_mrna_

15 all_x78926_1271-1812,hzf3_mrna_for_zinc_finger_protein_

x79568cds_1038-1314:in_reversesequence,_1399-1627,bdp1_mrna_for_protein-tyrosine-
phosphatase_

all_y00787_1314-1469,mrna_for_mdncf_(monocyte-derived_neutrophil_chemotactic_factor)_

all_z29074_1968-2269,mrna_for_cytokeratin_9

20 Metagene 377

d49488_640-1138,mrna_for_alpha-tocopherol_transfer_protein,_complete_cds_

134363cds_3540-3847:in_reversesequence,_4791-4896,x-

25 linked_nuclear_protein_(xnp)_gene,_complete_cds

l39064mrna_3922-4348,interleukinreceptor_(il9r)_gene,_complete_cds

m20218exon_15-249:not_in_gb_record,coagulation_factor_xi_gene_

m26665_267-484,histatin(his2)_mrna,_complete_cds,histatin(his2)_mrna,_complete_cds

m59499mrna#1_3549-3891,lipoprotein-associated_coagulation_inhibitor_(laci)_gene

30 m61176_1093-1549,brain-derived_neurotrophic_factor_(bdnf)_mrna,_complete_cds

u02632_2711-3047,calcium-activated_potassium_channel_mrna,_partial_cds_

u27193_1872-2346,protein-tyrosine_phosphatase_mrna,_complete_cds_

Metagene 96

35 hg2668-ht2764_at_hg2668-ht2764_bradykinin_receptor_

u58032_1007-

1322,myotubularin_related_protein(mtmr1)_gene,_partial_cds/gb=u58032_ntype=dna_annot=c

u89012_2087-2639,dentin_matrix_acidic_phosphoprotein(dmp1)_mrna,_complete_cds

Metagene 63

d55638_227-659,b-cell_pabl_(pseudoautosomal_boundary-
 5 like_sequence)_mrna,_clone_bc4/gb=d55638_/ntype
 d78261_1293-1433,icsat_transcription_factor_mrna,_partial_cds,_similar_to_mouse_pip/lisrf_(irf-
 4)_s
 hg1437-ht1437_s_at_hg1437-ht1437_proto-oncogene_trk
 hg2825-ht2949_at_hg2825-ht2949_ret_transforming_gene
 10 hg3570-ht3773_at_hg3570-ht3773_protein_phosphatase_inhibitor_homolog
 hg668-ht4793_at_hg668-ht4793_t-cell_factor_1,_a/b/c,_alts splice_1,_a
 j04430mrna_794-1350,tartrate-resistant_acid_phosphatase_type mrna,_complete_cds
 l08187_551-1079,cytokine_receptor_(ebi3)_mrna,_complete_cds
 l34059_2447-3017,cadherin-4_mrna,_complete_cds
 15 m37984mrna_97-589,slow_twitch_skeletal_muscle/cardiac_muscle_troponin_c_gene,_complete_cds
 m57506mrna_25-481,_scya1_gene_(secreted_protein_i-309)_extracted_from secreted_protein_(i-
 309)_gene,_
 m74089_1911-2271,tb1_gene_mrna,_3'_end_
 s77094_1075-
 20 1621,_nicotinic_acetylcholine_receptor_alpha_subunit|achr_alpha_subunit_[human,_thymic_c
 s80050mrna_653-1133,_udp-n-acetylglucosamine:_alpha-6-d-mannoside_beta-1,6-n-
 acetylglucosaminyltrans
 s82185_419-905,_brag-1=brain-related_apoptosis_gene/bcl-2_homolog_[human,_mg-
 107_glioma,_mrna_partia
 25 u00928_611-1151,clone_ce29_4.1_(cac)n(gtg)n_repeat-containing_mrna
 u09412_1619-2045,zinc_finger_protein_znf134_mrna,_complete_cds
 u11878_4-169,interleukin-
 8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb10,_partial_cds/gb=u118
 u12775exon_156-342:not_in_gb_record,agouti_gene
 30 u13022_1572-2124,negative_regulator_of_programmed_cell_death_ich-1s_(ich-
 1)_mrna,_complete_cds
 u15306_3076-3466,cysteine-rich_sequence-specific_dna-
 binding_protein_nfx1_mrna,_complete_cds
 u18259_6077-6647,clone_ciita-8_mhc_ii_transactivator_ciita_mrna,_complete_cds
 35 u22178_3-321,prostatic_secretory_protein_57_mrna,_complete_cds/gb=u22178_/ntype=rna
 u28488_1344-1847,putative_g_protein-coupled_receptor_(az3b)_mrna,_complete_cds
 u34877_511-997,biliverdin-ixalpha_reductase_mrna,_complete_cds
 u43959_758-815,betaadducin_mrna,_alternatively_spliced_partial_cds
 u77129_2447-2975,sps1/ste20_homolog_khs1_mrna,_complete_cds

u79247_1157-1559,clone_23599_mrna_sequence_
 u83115_6327-6753,non-lens_beta_gamma-crystallin_like_protein_(aim1)_mrna,_partial_cds
 u85430_3114-3279,transcription_factor_nfatx4_mrna,_complete_cds
 x04327mrna_1084-1564,erythrocyte_2,3-bisphosphoglycerate_mutase_mrna_ec_2.7.5.4
5 all_x13255_2280-2725,mrna_for_dopamine_beta-hydroxylase_type_a_(ec_1.14.17.1)
 x15393mrna_19-541,motilin_gene_exon(and_joined_cds)
 x59711cds_626-998:in_reversesequence,_1244-1280,mrna_for_caat-
 box_dna_binding_protein_subunit_a_
 x67337_2825-3365,hpbrii-4_mrna_
10 all_x69636_1268-1951,mrna_sequence_(15q11-13)
 all_x78933_1420-1970,hzf10_mrna_for_zinc_finger_protein
 x83441mrna_2724-3102,mrna_for_dna_ligase_iv
 all_x90568_81371-81864,mrna_for_titin_protein_(clone_hh1-hh54)_
 all_x91868_915-1378,mrna_for_six1_protein
15 all_x96754_846-1051,gene_encoding_kappa_light_chain_constant_region
 x98206mrna_55-277:in_reversesequence,_307,mrna_for_uv-
 b_repressed_sequence,_hur/gb=x98206_/ntype=rna

Metagene 77

20

u12767_4598-4922,mitogen_induced_nuclear_orphan_receptor_(minor)_mrna,_complete_cds
 u79298_928-1312,clone_23803_mrna,_partial_cds
 x58987mrna_1801-2299,mrna_for_d-1_dopamine_receptor
 all_x97671_31-566,mrna_for_erythropoietin_receptor_

25

Metagene 380

m27281_642-1116,vascular_permeability_factor_mrna,_complete_cds
 m75110_814-1312,h,k-atpase_beta_subunit_mrna,_complete_cds_
30 m99487_2039-2555,prostate-specific_membrane_antigen_(psm)_mrna,_complete_cds_
 u73704_1248-1764,48_kda_fkbp-associated_protein_fap48_mrna,_complete_cds

Metagene 229

35

m27160mrna_1441-1879,tyrosinase_(tyr)_mrna,_complete_cds_
 m64590_3317-3737,glycine_decarboxylase_mrna,_complete_cds
 u26712_2910-3318,cbl-b_truncated_formlacking_leucine_zipper_mrna,_complete_cds

Metagene 345

d00632_1032-1470,plasma_(extracellular)_mrna_for_glutathione_peroxidase,_complete_cds
d38145_1418-1952,mrna_for_prostacyclin_synthase,_complete_cds
s77812_148-

5 211,_flt=vascular_endothelial_growth_factor_receptor/vegf_receptor/cell_surface_tyrosine_u05861exon_50-243:not_in_gb_record,hepatic_dihydrodiol_dehydrogenase_gene_

Metagene 327

10 hg4167-ht4437_at_hg4167-ht4437_nuclear_factor_1,_a_type
hg855-ht855_s_at_hg855-ht855_dna_excision_repair_protein_ercc6_j05037_918-1368,serine_dehydratase_mrna,_complete_cds
j05401_1158-1554,sarcomeric_mitochondrial_creatine_kinase_(mtck)_gene,_complete_cds
146353mrna_6579-7077,high-mobility_group_phosphoprotein_(hmgi-c)_gene,_exons_3-jan
15 u10886_4762-5068,density_enhanced_phosphatase-1_mrna,_complete_cds_u22233_1659-2166,methylthioadenosine_phosphorylase_(mtap)_mrna,_complete_cds_all_x03350_1973-2514,mrna_for_alcohol_dehydrogenase_beta-1-subunit_(adh1-2_allele)_z94753exon_92-444:in_fullsequence,_1246-1265,dna_sequence_from_pac_465g10_on_chromosome_x_contains_m

20

Metagene 187

108835mrna#1_3166-
3367,_dm_kinase_gene_(myotonic_dystrophy_kinase)_extracted_frommyotonic_dystrophy_25 all_m19311_876-1059,calmodulin_mrna,_complete_cds,calmodulin_mrna,_complete_cds_u53506_1344-1836,type_ii_iodothyronine_deiodinase_mrna,_complete_cds.

Metagene 490

30 af005775_275-755,caspase-like_apoptosis_regulatory_protein(clarp)_mrna,_alternatively_spliced,_compl135269exon_1602-2040,zinc_finger_protein_35_(znf35)_gene_u32499_848-929,d3_dopamine_receptor_mrna,_complete_cds.
u78107_667-1105,gamma_snap_mrna,_complete_cds
35 u85946_2030-2288,brain_secretory_protein_hsec10p_(hsec10)_mrna,_complete_cds_

Metagene 484

ab003177_604-1096,mrna_for_proteasome_subunit_p27,_complete_cds

hg3187-ht3366_s_at_hg3187-ht3366_tyrosine_phosphatase_1,_non-receptor,_altslice_3_
 hg3546-ht3744_s_at_hg3546-ht3744_pre-mrna_splicing_factor_sf2p33,_altslice_form_1_
 m19650_1446-1700,2',3'-cyclic_nucleotide_3'-phosphodiesterase_mrna,_complete_cds
 s62904_2130-

5 2523_thiopurine_methyltransferase_[human,_t84_colon_carcinoma_cell,_mrna,_2742_nt]
 u47007_1818-2250,transcriptional_repressor_(nab1)_nab1_mrna,_complete_cds
 u51004_166-508,putative_protein_kinase_c_inhibitor_(pkci-1)_mrna,_complete_cds_
 u90304_1272-1782,iroquois-class_homeodomain_protein_irx-2a_mrna,_complete_cds
 z93784cds_702-

10 1008:in_reversesequence,_58791:not_in_gb_record,dna_sequence_from_pac_398c22_on_chromo

Metagene 480

d38500_574-958,pms6_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-terminal_region

15 hg1751-ht1768_s_at_hg1751-ht1768_chorionic_somatotropin_hormone_cs-5
 hg1783-ht1803_s_at_hg1783-ht1803_islet_amyloid_polypeptide
 hg4116-ht4386_s_at_hg4116-ht4386_olfactory_receptor_or17-219
 l14813_856-1147,carboxyl_este_lipase_like_protein_(cell)_mrna,_complete_cds

20 176703mrna_2687-3245,b56epsilon_mrna,_complete_cds
 m26856cds_1126-1456:in_reversesequence,_3467-3600,21-hydroxylase_b_gene,_complete_cds_all_m60746_531-844,histone_h3.1_(h1f3)_gene,_complete_cds
 s52028_582-1141,cystathione_gamma-lyase_{clone_hcl-1}_{[human,_liver,_mrna,_1194_nt]}
 s68271_891-1191,crem=cyclic_amp-responsive_element_modulator_[human,_mrna,_1431_nt]

25 u03886_2214-2730,gs2_mrna,_complete_cds
 u10685exon#2_992-1142:in_reversesequence,_3043-3271,mage-10_antigen_(mage10)_gene,_complete_cds_u47050_2888-3296,putative_calcium_influx_channel_(htrp3)_mrna,_complete_cds
 u49114_2196-2700,prohormone_convertaseprecursor_(pc5)_mrna,_partial_cds

30 u58522_1608-2124,huntingtin_interacting_protein_(hip2)_mrna,_complete_cds
 u66036_732-1236,sulfotransferase_mrna,_complete_cds
 u74382_1317-1900,telomeric_repeat_dna-binding_protein_(pin2)_mrna,_complete_cds
 u84573_2882-3422,lysyl_hydroxylase_isoform(plod2)_mrna,_complete_cds_u87593_f_at_u87593_u87593_4040_in_u87593_31-

35 568,endogenous_retrovirus_clone_p1.8_polymerase_mrna,_p
 all_x16546_724-1319,dna_for_eosinophil_derived_neurotoxin
 x17576cds_802-1078:in_reversesequence,_1233-
 1389,melanoma_mrna_for_nck_protein,_showing_homology_to
 all_z22970_4355-4674,mrna_for_m130_antigen_cytoplasmic_variant_2_

Metagene 477

ab000897_43-373,mrna_for_cadherin_fib3,_partial_cds/gb=ab000897/_ntype=rna
 5 hg3033-ht3194_at_hg3033-ht3194_spliceosomal_protein_sap_62_
 hg3426-ht3610_s_at_hg3426-ht3610_zinc_finger_protein_hzf-16,_kruppel-like,_alts splice_1_
 l24559_1634-2078,dna_polymerase_alpha_mrna,_complete_cds
 u07139_2039-2459,voltage-gated_calcium_channel_beta_subunit_mrna,_complete_cds
 u36500_2741-3209,lymphoid-specific_sp100_homolog_(lysp100-b)_mrna,_complete_cds
 10 u46767_288-768,monocyte_chemoattractant_protein-4_precursor_(mcp-4)_mrna,_complete_cds_
 all_u60269_13-524,endogenous_retrovirus_herv-
 k(hml6)_proviral_clone_hml6.17_putative_polymerase_and_
 x76223exon_2-540,mal_gene_exon_4.
 x89267exon#10_225-
 15 312,dna_for_uroporphyrinogen_decarboxylase_gene/gb=x89267/_ntype=dna/_annot=exon_
 x90978_1187-1751,mrna_for_an_acute_myeloid_leukaemia_protein_(1793bp)

Metagene 467

20 d38502_850-1120,pms4_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-terminal_regio
 d84145_458-980,ws-3_mrna,_complete_cds_
 hg1828-ht1857_at_hg1828-ht1857_nexin,_glia-derived_
 hg3513-ht3707_at_hg3513-ht3707_myosin,_heavy_polypeptide,_light_meromyosin_
 25 hg3954-ht4224_s_at_hg3954-ht4224_landsteiner-wiener_blood_group_glycoprotein_(lw)
 hg4114-ht4384_at_hg4114-ht4384_olfactory_receptor_or17-209_
 reverse_j04742_384-607:in_j04742cds_49-110,autonomous_replicating_sequence_h1_(arsh1)_
 l03785_72-582,regulatory_myosin_light_chain_(myl5)_mrna,_complete_cds
 all_l26336_2691-3220,heat_shock_protein_hspa2_gene,_complete_cds_
 30 l35253_972-1047,p38_mitogen_ACTIVATED_protein_(map)_kinase_mrna,_complete_cds
 l40388mrna_195-
 675,thyroid_receptor_interactor_(trip15)_mrna,_5'_end_of_cds/gb=l40388/_ntype=rna
 all_m21388_2-95,unproductively_rearranged_ig_mu-chain_mrna_v-region_(vd),_5'_end,_clone_mu-
 3a1a.,unp
 35 m21984_441-951,(clone_pwhtnt16)_skeletal_muscle_troponin_t_mrna,_complete_cds
 m31523_4155-4353,transcription_factor_(e2a)_mrna,_complete_cds_
 m33653_467-965,(clones_ht-[125,133])_alpha-2_type_iv_collagen_(col4a2)_mrna,_complete_cds
 m62840mrna_1755-2175,acyloxyacyl_hydrolase_mrna,_complete_cds
 m65134mrna_3588-4102,complement_component_c5_mrna,_3'_end

m90391_1736-2866,putative_il-16_protein_precursor,_mrna,_complete_cds
 s66427_4218-4764,_rbp1=retinoblastoma_binding_protein[human,_nalm-6_pre-
 b_cell_leukemia,_mrna,_4834_

5 s70609_1781-2339,_glycine_transporter_type_1b_[human,_substantia_nigra,_mrna,_2364_nt]
 s81264_50-243,_hs-tbx2=t-box_gene_{t-
 box_region}{[human,_fetal_kidney,_mrna_partial,_283_nt]/gb=s812
 u03486cds_625-1045:in_reversesequence,_1121-1211,connexin40_gene,_complete_cds
 u06632_2039-2579,p80-coilin_mrna,_complete_cds_

10 u16997_1218-1764,orphan_receptor_ror_gamma_mrna,_complete_cds
 u19487_1843-2329,prostaglandin_e2_receptor_mrna,_complete_cds
 u21936_2630-3038,peptide_transporter_(hpept1)_mrna,_complete_cds_

15 u27459_2534-2984,origin_recognition_complex_proteinhomolog_horc2l_mrna,_complete_cds
 u43318_1805-2291,putative_transmembrane_receptor_(frizzled_5)_mrna,_complete_cds_

20 u51010exon_17-222,nicotinamide_n-
 methyltransferase_gene,_exonand_5'_flanking_region/gb=u51010/_ntype
 u59289_3350-3824,h-cadherin_mrna,_complete_cds_

25 u61374_1265-
 1715,novel_protein_with_short_consensus_repeats_of_six_cysteines_mrna,_complete_cds
 u61836mrna_540-972,putative_cyclin_g1_interacting_protein_mrna,_partial_sequence_

30 u62317mrna#7_2016-
 2532,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_cit
 u66617_2252-
 2786,swi/snf_complex_60_kda_subunit_(baf60a)_mrna,_alternatively_spliced,_complete_cds_

35 u78027mrna#4_1964-2372,_l441_gene_(l44-
 like_ribosomal_protein)_extracted_frombruton_tyrosine_kinase_
 u82256_1325-1823,arginase_type_ii_mrna,_complete_cds_

40 u82303_25-313,unknown_protein_mrna,_partial_cds/gb=u82303/_ntype=rna_

45 u95020_1276-1786,voltage-dependent_calcium_channel_beta-4_subunit_mrna,_complete_cds.
 x04898mrna_49-445,gene_for_apolipoprotein_aII_

50 30 all_x52056_778-1304,mrna_for_spi-1_proto-oncogene
 x59770mrna_685-1213,il-1r2_mrna_for_type_ii_interleukin-1_receptor,(cell_line_cb23)_
 x61177mrna_1495-1933,hsil5r2_gene_for_interleukin-5_receptor_type_2
 x79780cds_94-622:in_reversesequence,_646,ypt3_mrna
 all_z35085_1960-2506,mrna_for_unknown_antigen

55 35 z47055cds_437-968,partial_cdna_sequence,_farnesyl_pyrophosphate_synthetase_like-
 4/gb=z47055/_ntype=d

d21853_1111-1543,mrna_for_kiaa0111_gene,_complete_cds
 d79986_4973-5513,mrna_for_kiaa0164_gene,_complete_cds
 d87077_5465-5975,mrna_for_kiaa0240_gene,_partial_cds_
 hg3076-ht3238_s_at_hg3076-ht3238_heterogeneous_nuclear_ribonucleoprotein_k,_altslice_1
5 hg3514-ht3708_at_hg3514-ht3708_tropomyosin_tm30nm,_cytoskeletal
 hg4322-ht4592_at_hg4322-ht4592_tubulin,_beta_
 j02621mrna_653-1214,non-histone_chromosomal_protein_hmg-14_mrna,_complete_cds
 j04029_1450-2007,keratintype_i_intermediate_filament_(krt10)_mrna,_complete_cds_
 j04152mrna_1181-1648,_m1s1_gene_extracted_fromgastrointestinal_tumor-
10 associated_antigen_ga733-1_prot
 l37368_1849-2359,(clone_e5.1)_rna-binding_protein_mrna,_complete_cds_
 l40397mrna_979-1267,(clone_s31i125)_mrna,_3'_end_of_cds_
 l42379mrna_2645-3155,bone-derived_growth_factor_(bpgf-1)_mrna,_complete_cds_
 m16342mrna#2_1287-
15 1581,nuclear_ribonucleoprotein_particle_(hnrrnp)_c_protein_mrna,_complete_cds_
 m19311mrna_520-1052,calmodulin_mrna,_complete_cds,calmodulin_mrna,_complete_cds_
 m23379_3723-4179,gtpase-activating_protein_ras_p21_(rasa)_mrna,_complete_cds_
 u00947_1301-1347,clone_c4e_3.2_(cac)n/(gtg)n_repeat-containing_mrna
 u06631_3269-3779,(h326)_mrna,_complete_cds_
20 u20998_973-1417,signal_recognition_particle_subunit(srp9)_mrna,_complete_cds_
 u35048_1159-1675,tsc-22_protein_mrna,_complete_cds_
 u35451_1643-2027,heterochromatin_protein_p25_mrna,_complete_cds
 u57877_766-1144,integral_membrane_protein_cii-
 3_mrna,_nuclear_gene_encoding_mitochondrial_protein,_c
25 u77948_2714-3236,bruton_tyrosine_kinase-associated_protein-135_mrna,_complete_cds
 u79282_1087-1651,clone_23801_mrna_sequence_
 u90549_1452-1932,non-histone_chromosomal_protein_(nhc)_mrna,_complete_cds
 u90551_1071-1623,histone_2a-like_protein_(h2a/l)_mrna,_complete_cds
 u95740mrna#1_5316-
30 5856,_362g6.1_gene_(unknown_protein_cit987sk_362g6_1)_extracted_fromchromosome_16p
 x01703exon#4_929-1151,gene_for_alpha-tubulin_(b_alpha_1)_
 x15729cds_1538-1820:in_reversesequence,_2069-2215,mrna_for_nuclear_p68_protein
 x59405exon#12_1560-2040,_h.sapiens,_gene_for_membrane_cofactor_protein
 all_x63753_5116-5621,son-a_mrna
35 all_x68194_1513-2090,h-sp1_mrna
 all_x72841_1378-1937,ief_7442_mrna_
 all_x74104_650-1059,mrna_for_trap_beta_subunit_
 all_x75304_9705-10252,giantin_mrna_
 x81003mrna_1032-1560,hcg_v_mrna

all_x81198_3084-3673,mrna_(clone_p5)_for_archain
 all_x81625_3058-3617,mrna_for_c11_protein
 all_x84908_3722-3975,mrna_for_phosphorylase-kinase,_beta_subunit
 all_x86098_2367-2704,mrna_for_bs69_protein
5 all_x95648_1063-1658,mrna_for_eif-2b_alpha_subunit
 all_z72499_3157-3740,mrna_for_herpesvirus_associated_ubiquitin-specific_protease_(hausp).

Metagene 446

10 d17391_2957-3497,mrna_for_alpha_4(iv)_collagen,_c-terminal
 hg4582-ht4987_at_hg4582-ht4987_glucocorticoid_receptor,_beta_
 104569_8323-8890,(clone_hht-1)_1-type_voltage-
 dependent_calcium_channel_a1_subunit_(hht)_mrna,_compl
 m37815mrna#1_1079-1589,_cd28_gene_(glycoprotein_cd28)_extracted_fromt-
15 cell_membrane_glycoprotein_cd2
 z49995mrna_2014-2590,mrna_(non-coding;_clone_h2a)

Metagene 435

20 d14874_908-1406,mrna_for_adrenomedullin,_complete_cds
 d50857_5954-6440,dock180_protein_mrna,_complete_cds
 hg1428-ht1428_s_at_hg1428-ht1428_globin,_beta
 hg2815-ht2931_s_at_hg2815-ht2931_myosin,_light_chain,_alkali,_smooth_muscle,_non-
 muscle,_altssplice_2
25 hg3523-ht4899_s_at_hg3523-ht4899_proto-oncogene_c-myc,_alts splice_3,_orf_114
 l09235_1323-1845,vacuolar_atpase_(isoform_va68)_mrna,_complete_cds
 l10838_79-499,sr_protein_family,_pre-mrna_splicing_factor_(srp20)_mrna,_complete_cds
 l42601cds_1334-1665:in_reversesequence,_247-470,keratinisoform_k6c_(krt6c)_gene_
 m81637_1078-1603,grancalcin_mrna,_complete_cds
30 s82297_3-391,_beta_2-microglobulin_{11bp_deleted_between_nucleotides_98-
 99}_{human,_colon_cancer_cel
 u07158_641-1169,syntaxin_mrna,_complete_cds
 u37518_1162-1390,tnf-related_apoptosis_inducing_ligand_trail_mrna,_complete_cds
 u43083_1408-1582,g_alpha-q_(gaq)_mrna,_complete_cds
35 u84569_647-1217,yf5_mrna,_complete_cds
 u91327mrna_156-654,chromosome_12p15_bac_clone_cit987sk-
 99d8_complete_sequence/gb=u91327/_ntype=dna/_
 x03689cds_17-255,mrna_fragment_for_elongation_factor_tu_(n-terminus)/gb=x03689/_ntype=rna
 x89399_s_at_x89399_x89399,not_in_gb_record,mrna_for_ins(1,3,4,5)p4-binding_protein

x95073_657-1119,mrna_for_translin_associated_protein_x_

Metagene 404

5 d87009cds#5_1325-1565:in_fullsequence,_35519-
 35735,_5'_oy11.1_gene_extracted_from(lambda)_dna_for_im
 m68895mrna_858-1278,alcohol_dehydrogenasegene,_complete_cds
 x54489mrna_660-1034,gene_for_melanoma_growth_stimulatory_activity_(mgsa)
 all_x68242_408-889,mrna_for_hin-1

10

Metagene 338

d50370_2047-2581,mrna_for_nucleosome_assembly_protein,_complete_cds
 143576_709-1009,(clone_est02946)_mrna_

15 m36118_491-828,cytotoxin_serine_protease-c_mrna,_complete_cds
 s81419_25-
 349,_dystrophin,_dystrophin_{purkinje_promoter,_alternatively_spliced}_{[human,_cortical_br
 u04735_1728-2184,microsomal_stress_70_protein_atpase_core_(stch)_mrna,_complete_cds
 u45255mrna_1576-1952,paired-box_protein_pax2_(pax2)_gene_-

20 u58331_762-1041,placental_delta_sarcoglycan_mrna,_complete_cds_-
 u63139_5305-5779,rad50_(rad50)_mrna,_complete_cds
 x92110mrna_714-1242,mrna_for_hcgviii_protein_-
 z47553mrna_1761-2247,mrna_for_flavin-containing_monooxygenase(fmo5)_

25 Metagene 316

hg172-ht3924_at_hg172-ht3924_spermidine/spermine_n1-acetyltransferase,_altslice_2_-
 s79267_2828-3398,_cd4_receptor_{exonsand_2}_{[human,_t-lymphocyte,_mrna,_3429_nt]}_-
 u10868_2267-2765,aldehyde_dehydrogenase_aldh7_mrna,_complete_cds_-

30 u31449_773-1337,intestinal_and_liver_tetraspan_membrane_protein_(il-tmp)_mrna,_complete_cds
 u57911_1693-2203,fetal_brain_(239fb)_mrna,_from_the_wagr_region,_complete_cds
 u67934cds_375-501:in_reversesequence,_549-
 765,44.9_kda_protein_c18b11_homolog_gene,_partial_cds
 x58022mrna_803-1223,mrna_for_corticotropin-releasing_factor_binding_protein_(crf-bp)_

35

Metagene 299

s75881_234-719,_a-myb-dna-binding_transactivator_{3'_region}_{[human,_ccrf-cem_t-
 leukemia_line,_mrna_}

z21707cds_552-912:in_reversesequence,_954-984,p18_mrna

Metagene 298

- 5 d64110_615-1161,mrna_for_tob_family,_complete_cds
hg2564-ht2660_s_at_hg2564-ht2660_gamma-aminobutyric_acid_(gaba)_a_receptor,_alpha_subunit
j04056_746-1118,carbonyl_reductase_mrna,_complete_cds
m64174_3012-3468,protein-tyrosine_kinase_(jak1)_mrna,_complete_cds_
u82319_470-980,clone_ydd19_mrna_sequence_
- 10 x67594cds_507-909:in_reversesequence,_1119-1221,mrna_for_msh_receptor_

Metagene 296

- m69177_1992-2436,monoamine_oxidase_b_(maob)_mrna,_complete_cds_
- 15 m94151_3127-3631,cadherin-associated_protein-related_(cap-r)_mrna,_complete_cds
u01102exon#1-3_4-
109:not_in_gb_record,lung_clara_cellskda_secretory_protein_(cc10)_gene,_satellite_a
u49835_832-1361,ykl-39_precursor_mrna,_complete_cds
u88898_561-757,endogenous_retroviral_h_protease/integrase-
20 derived_orf1_mrna,_complete_cds,_and_putat

Metagene 277

- ac000066cds_2985-3237:in_reversesequence,_48519-48663,bac_clone_rg293f11_from_7q21-7q22_
- 25 af000560_1220-1697,ttf-i_interacting_peptidemrna,_partial_cds.
d86958_6175-6430,mrna_for_kiaa0203_gene,_complete_cds
hg3369-ht3546_at_hg3369-ht3546_potassium_channel,_voltage-gated,_isk-related_family,_member_1
143575mrna_1021-1106,(clone_48a8)_mrna
- 30 m15841_492-945,u2_small_nuclear_rna-associated_b"抗原_mrna,_complete_cds
m27878_2656-3172,dna_binding_protein_(hpf2)_mrna,_complete_cds_
m31516mrna_1492-2002,decay-accelerating_factor_mrna,_complete_cds
m34309_4410-4836,epidermal_growth_factor_receptor_(her3)_mrna,_complete_cds
m99436_1808-2246,transducin-like_enhancer_protein_(tle2)_mrna,_complete_cds
- 35 u18242_761-1265,calcium_modulating_cyclophilin_ligand_(camlg)_mrna,_complete_cds_
u51334_1840-2068,putative_rna_binding_protein_(rbp56)_mrna,_complete_cds_
u60205_1192-1726,methyl_sterol_oxidase_(erg25)_mrna,_complete_cds
u65928_711-1125,jun_activation_domain_binding_protein_mrna,_complete_cds_
u82279_1505-2069,immunoglobulin-like_transcriptmrna,_complete_cds_

u91521_2098-2470,peroxin(hspex12)_mrna,_complete_cds.
 all_x79353_1624-2189,xap-4_mrna_for_gdp-dissociation_inhibitor_
 all_x80754_1279-1862,mrna_for_gtp-binding_protein
 x81851cds_26-326,_hsapiens_il-4_gene_splice_variant/gb=x81851/_ntype=ma
5 all_x83543_7066-7427,apx1_mrna_
 x90999cds_390-726:in_reversesequence,_828-942,mrna_for_glyoxalase_ii
 all_x99584_197-630,mrna_for_smt3a_protein
 all_y00291_2443-2888,hap_mrna_encoding_a_dna-binding_hormone_receptor
 all_y07566_951-1066,mrna_for_rit_protein_

10

Metagene 270

d45917_634-1120,mrna_for_timp-3,_partial_cds_(c-terminus_region)_
 d83174_1524-1896,mrna_for_collagen_binding_protein_2,_complete_cds_
15 d86479_2250-2814,mrna_for_aebp1_gene,_complete_cds_
 d87258_1489-1999,cancellous_bone_osteoblast_mrna_for_serin_protease_with_igf-
 binding_motif,_complete
 hg2197-ht2267_s_at_hg2197-ht2267_collage,_type_vii,_alpha_1
 hg3543-ht3739_at_hg3543-ht3739_insulin-like_growth_factor_
20 hg987-ht987_at_hg987-ht987_mac25_
 j02611mrna_208-766,apolipoprotein_d_mrna,_complete_cds_
 j03040_1508-2000,sparc/osteonectin_mrna,_complete_cds
 j03278_5029-5485,platelet-derived_growth_factor_(pdgf)_receptor_mrna,_complete_cds_
 l32137_1910-2309,germline_oligomeric_matrix_protein_(comp)_mrna,_complete_cds
25 l36033_2929-3343,pre-b_cell_stimulating_factor_homologue_(sdf1b)_mrna,_complete_cds
 m11718_716-1274,alpha-2_type_v_collagen_gene,_3'_end_
 m16279mrna_757-1153,mic2_mrna,_complete_cds
 m25269_1791-2211,tyrosine_kinase_(elk1)_oncogene_mrna,_complete_cds_
 m55593mrna#1_2600-2936,collagenase_type_iv_(clg4)_gene_
30 m85289_14032-14302,heparan_sulfate_proteoglycan_(hsgp2)_mrna,_complete_cds_
 m96233exon#8_114-467,glutathione_transferase_mu_number(gstm4)_gene,_complete_cds
 all_u14394_4004-4533,tissue_inhibitor_of_metalloproteinases-3_mrna,_complete_cds_
 u16306_10722-11142,chondroitin_sulfate_proteoglycan_versican_v0_splice-
 variant_precursor_peptide_mrn
35 u24389cds_1495-1696:in_reversesequence,_207-339:not_in_gb_record,lysyl_oxidase-
 like_protein_gene_
 u60115_1863-2211,skeletal_muscle_lim-protein_slim1_mrna,_complete_cds
 u77846mrna_979-
 1356,elastin_gene,_partial_cds_and_partial_3'_utr,elastin_gene,_partial_cds_and_parti

all_x15880_1690-2273,mrna_for_collagen_vi_alpha-1_c-terminal_globular_domain_x15882cds_984-1230:in_reversesequence,_1272-1554,mrna_for_collagen_vi_alpha-2_c-terminal_globular_do
 x79683cds_4908-5361:in_reversesequence,_5594-5620,lamb2_mrna_for_beta2_laminin
5 x86693mrna_2171-2675,mrna_for_hevin_like_protein_z48199exon#4_1510-2026,syndecan-1_gene_(exons_2-5)_z49269exon#1-3_76-199:not_in_gb_record,gene_for_chemokine_hcc-1_

Metagene 265

10
 d84110_1113-1515,mrna_for_werner_syndrome-1/type_4,_complete_cds_d86982_5824-6286,mrna_for_kiaa0229_gene,_partial_cds_hg4518-ht4921_at_hg4518-ht4921_transcription_factor_btf3_homolog_x04085mrna_1684-
15 2236,gene_for_catalase_(ec_1.11.1.6)_5'_flank_and_exonmapping_to_chromosome_11,_band x67098exon#8_40-454,rtt_alpha_mrnaContaining_four_open_reading_frames_

Metagene 247

20 d86983_5131-5485,mrna_for_kiaa0230_gene,_partial_cds_hg142-ht142_at_hg142-ht142_modulator_recognition_factor_hg3995-ht4265_at_hg3995-ht4265_cpg-enriched_dna,_clone_s19_j04599_1078-1630,hpgi_mrna_encoding_bone_small_proteoglycan_i_(biglycan),_complete_cds_j05243_7216-7732,nonerythroid_alpha-spectrin_(sptan1)_mrna,_complete_cds
25 l06139_3573-4083,receptor_protein-tyrosine_kinase_(tek)_mrna,_complete_cds l41143_1635-2085,expressed_pseudo_tcta_mrna_at_t(1;3)_translocation_site,_complete_cds m13194mrna_586-1006,excision_repair_protein_(ercc1)_mrna,_complete_cds,_clone_pcde_ m25079_163-230,sickle_cell_beta-globin_mrna,_complete_cds m57609mrna_4490-5012,dna-binding_protein_(gli3)_mrna,_complete_cds_

30 x15306mrna_3269-3707,nf-h_gene,_exon(and_joined_cds)_x75546cds_626-926:in_reversesequence,_1204,mrna_for_fibromodulin z83799_15-239,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc1). all_z84721_30317- 34635,dna_sequence_from_cosmid_gg1_from_a_contig_from_the_tip_of_the_short_arm_of_c

35
Metagene 243

m60974_731-1304,growth_arrest_and_dna-damage-inducible_protein_(gadd45)_mrna,_complete_cds_

all_x14894_826-1385,mrna_for_myogenic_factor_myf-5_

Metagene 242

- 5 d10704_1969-2365,mrna_for_choline_kinase_

d13413mrna_578-617,mrna_for_tumor-

associated_120_kda_nuclear_protein_p120,_partial_cds(carboxyl_term

d13900_748-1234,mrna_for_mitochondrial_short-chain_enoyl-coa_hydratase,_complete_cds_

d64108_1595-2079,mrna_for_dmc1_homologue,_complete_cds_
- 10 hg3999-ht4269_at_hg3999-ht4269_retinoic_acid_receptor_beta,_isoform_1_

j03071cds#3_151-604:in_reversesequence,_14327-28953,_growth_hormone_gh-

1_gene_extracted_fromgrowth_h

113042exon#2-3_11-216:not_in_gb_record,calbindin_d-9k_gene,_5'_end_cds_

114778_1665-2225,calmodulin-
- 15 dependent_protein_phosphatase_catalytic_subunit_(ppp3ca)_mrna,_complete_

137043mrna_742-1294,casein_kinase_i_epsilon_mrna,_complete_cds

146720cds_2231-2557:in_reversesequence,_2650-2828,autotaxin-t_(atx-t)_gene,_complete_cds

all_m55420_605-897:in_m55420cds_109-140,ige_chain,_lastexons_

m63904mrna_1519-2029,g-alphaprotein_mrna,_complete_cds_
- 20 m65066_1903-2323,camp-dependent_protein_kinase_regulatory_subunit_ri-beta_mrna,_3'_end_

m75099_25-493,rapamycin- and_fk506-binding_protein,_complete_cds_

m87338_1120-1660,replication_factor_40-kda_subunit_(a1)_mrna,_complete_cds

s68616_4005-4491,_na+/h+_exchanger_nhe-1_isoform_[human,_heart,_mrna,_4516_nt]

u20530_47-593,bone_phosphoprotein_spp-
- 25 24_precursor_mrna,_complete_cds/gb=u20530_/ntype=rna_

u22398_1030-1468,cdk-inhibitor_p57kip2_(kip2)_mrna,_complete_cds_

u33839_at_u33839_u33839,not_in_gb_record,potassium_channel_mrna,_complete_cds/gb=u33839_/

ntype=rna_

u61262_4667-5195,neogenin_mrna,_complete_cds_
- 30 u66619_1165-1699,swi/snf_complex_60_kda_subunit_(baf60c)_mrna,_complete_cds

u82313_133-439,unknown_protein_mrna,_partial_cds/gb=u82313_/ntype=rna

x69391cds_395-821,mrna_for_ribosomal_protein_l6

all_x82693_134-681,mrna_for_e48_antigen
- 35 Metagene 241

d83735_1551-2085,adult_heart_mrna_for_neutral_calponin,_complete_cds_

j04182_1914-2394,lysosomal_membrane_glycoprotein-1_(lamp1)_mrna,_complete_cds_

all_108895_3518-4059,mads/mef2-family_transcription_factor_(mef2c)_mrna,_complete_cds_

m19267_1476-1600,tropomyosin_mrna,_complete_cds
 all_m19481_278-651:in_m19481cds_818-921,follistatin_gene
 m21574mrna_5807-6293,platelet-derived_growth_factor_receptor_alpha_(pdgfra)_mrna,_complete_cds_

5 m74719_1971-2475,sef2-1b_protein_(sef2-1b)_mrna,_complete_cds
 m95787_494-1004,22kda_smooth_muscle_protein_(sm22)_mrna,_complete_cds
 s57132_3108-
 3615,_col16a1-type_xvi_collagen_alphachain_[human,_placenta,_mrna_partial,_3720_nt]
 s73591_2169-2649,_brain-expressed_hhcpa78_homolog_[human,_hl-

10 60_acute_promyelocytic_leukemia_cells,_
 u26710_3398-3878,cbl-b_mrna,_complete_cds
 u44975_791-1301,dna-binding_protein_cpbp_(cpbp)_mrna,_partial_cds
 u53446_2680-3220,mitogen-responsive_phosphoprotein_doc-2_mrna,_complete_cds
 u82532_231-753,gdi-dissociation_inhibitor_rhogdiggamma_mrna,_complete_cds

15 u90913_659-1157,clone_23665_mrna_sequence
 all_x13839_768-1300,mrna_for_vascular_smooth_muscle_alpha-actin
 all_x86809_1916-2367,mrna_for_major_astrocytic_phosphoprotein_pea-15_
 y12670mrna_531-1011,ob-rgrp_gene/gb=y12670_/ntype=rna
 all_z24727_1355-1569,tropomyosin_isoform_mrna,_complete_cds

20 z26248cds_178-640:in_reversesequence,_1512,mrna_for_eosinophil_granule_major_basic_protein
 all_z48923_3300-3835,mrna_for_bmpr-ii

Metagene 240

25 hg491-ht491_at_hg491-ht491_fc_receptor_iib3_for_igg_low_affinity
 m73720mrna_1032-1584,mast_cell_carboxypeptidase_a_(mc-cpa)_gene
 m82919_1201-1579,gamma_amino_butyric_acid_(gabaa)_receptor_beta-
 3_subunit_mrna,_complete_cds_
 u27109_3633-4155,prepromultimerin_mrna,_complete_cds_

30

Metagene 203

d50582cds_954-1128:in_reversesequence,_1367-
 1535,gene_for_inward_rectifier_k_channel,_complete_cds_
 35 hg2365-ht2461_at_hg2365-ht2461_glyceraldehyde-3-phosphate_dehydrogenase
 hg4188-ht4458_at_hg4188-ht4458_n-methyl-d-aspartate_receptor_subunit,_splice_variant_hnrln_
 j00146_388-718,dihydrofolate_reductase_pseudogene_(psi-hd1)
 l23808_1297-1717,metalloproteinase_(hme)_mrna,_complete_cds
 l27071_1963-2527,tyrosine_kinase_(txk)_mrna,_complete_cds

137378mrna_3182-3680,guanylyl_cyclase_(retgc-2)_mrna,_complete_cds
 140380mrna_285-795,thyroid_receptor_interactor_(trip11)_mrna,_3'_end_of_cds_
 all_148728_380-
 657:not_in_gb_record,_tcrbv10s1_gene_extracted_fromt_cell_receptor_beta_(tcrbv10s1)_g
5 m18079cds_85-343:in_reversesequence,_4158-
 4278,_human,_intestinal_fatty_acid_binding_protein_gene,_c
 m23234mrna_3313-3865,membrane_glycoprotein_p_(mdr3)_mrna,_complete_cds_
 m29386mrna_200-701,prolactin_mrna,_3'_end
 m94633exon_1275-
10 1611,recombination_acitivating_protein_(rag2)_gene,_last_exon/gb=m94633_/ntype=dna/_
 s77763_1132-
 1624,_nuclear_factor_erythroidisoform_f=basic_leucine_zipper_protein_{alternatively_spli
 all_u07807_3319-4740:in_u07807cds_13-110,metallothionein_iv_(mtiv)_gene,_complete_cds
 u10687exon#10_1056-1412,mage-4a_antigen_(mage4a)_gene,_complete_cds
15 u11690_3665-4241,faciogenital_dysplasia_(fgd1)_mrna,_complete_cds
 u13948_3283-3787,zinc_finger/leucine_zipper_protein_(af10)_mrna,_complete_cds
 u19345_2258-2756,arl_protein_(ar)_mrna,_complete_cds_
 u26174_499-991,pre-granzymemrna,_complete_cds_
 u33017_1248-1680,signaling_lymphocytic_activation_molecule_(slam)_mrna,_complete_cds_
20 u35459_629-1109,bomapin_mrna,_complete_cds/gb=u35459_/ntype=rna
 u52521_753-1131,arfaptin_1,_putative_target_protein_of_adp-
 ribosylation_factor,_mrna,_complete_cds_
 u72671_2390-2930,telencephalin_precursor_mrna,_complete_cds
 u96115_162-594,ww_domain-containing_protein_wwp3_mrna,_partial_cds/gb=u96115_/ntype=rna_
25 x12453mrna_993-1539,mrna_for_retinal_s-antigen_(48_kda_protein)
 all_x12530_1083-1415,mrna_for_b_lymphocyte_antigen_cd20_(b1_bp35)_
 x17648cds#2_1069-1177:in_reversesequence,_1341-1605,mrna_for_granulocyte-
 macrophage_colony-stimulati
 all_x17651_829-1412,myf-4_mrna_for_myogenic_determination_factor_
30 all_x52520_2414-2673,mrna_for_tyrosine_aminotransferase_(tat)_(ec_2.6.1.5)_
 x54131mrna_5534-6026,hptp_beta_mrna_for_protein_tyrosine_phosphatase_beta
 x57303cds_1488-1866:in_reversesequence,_2022-2028,rec11_mrna
 x61615cds_2830-3160:in_reversesequence,_3482-
 3548,mrna_for_leukemia_inhibitory_factor_(lif)_receptor
35 x65550exon#15_2051-2549,mki67a_mrna_(long_type)_for_antigen_of_monoclonal_antibody_ki-
 67_-
 all_y10032_1065-1588,mrna_for_putative_serine/threonine_protein_kinase_
 all_z29067_1423-1802,nek3_mrna_for_protein_kinase
 z30425cds_649-1009:in_reversesequence,_1299-1311,mrna_for_orphan_nuclear_hormone_receptor.

z35491mrna_797-1253,mrna_for_novel_glucocorticoid_receptor-associated_protein

Metagene 199

- 5 ac002086cds_1686-1974:in_reversesequence,_98485,pac_clone_dj525n14_from_xq23
k03218cds_1068-1587:in_reversesequence,_197-230,c-src-1_proto-oncogene
117418exon_3-
229;not_in_gb_record,_complement_receptorgene_extracted_fromcomplement_receptor_type(al
126953_2282-2846,chromosomal_protein_mrna,_complete_cds
- 10 u96136_4729-5233,delta-catenin_mrna,_complete_cds

Metagene 194

- 136642mrna_3940-4474,receptor_protein-tyrosine_kinase_(hek11)_mrna,_complete_cds
- 15 l78833cds#3_363-645:in_fullsequence,_17171-
17279,_brca1_gene_extracted_frombrca1,_rho7_and_vati_gene
m81886_2390-2861,glutamate_receptor_type(hbgr1)_mrna,_complete_cds
all_u17579_1465-1982,_growth_hormone-
releasing_hormone_receptor_form_b_gene_extracted_fromgrowth_hor

20

Metagene 193

- d78334_496-1018,mrna_for_ankyrin_motif,_complete_cds_
- u59228_407-797,ectodermal_dysplasia_protein_(eda)_mrna,_complete_cds_
- 25 x07384cds_2933-3269:in_reversesequence,_3377-3527,mrna_for_gli_protein
all_x73608_2895-3478,mrna_for_testican_

Metagene 189

- 30 af000562_43-427,uroplakin_ii_mrna,_partial_cds
d63134mrna_73-439,mrna_for_ets-like_30_kda_protein/gb=d63134_/ntype=rna
all_j00220_1704-1849,ig_germline_h-chain_g-e-a_region_a:_gamma-3_5'_flank,ig_germline_h-
chain_g-e-a_
all_j05253_8895-9496,interstitial_retinol-binding_protein_(irbp)_gene,_complete_cds
- 35 l37792mrna_1565-2015,syntaxin_1a_mrna,_complete_cds
all_m23533_3030-3556,alphaadrenergic_receptor_gene,_complete_cds
m29610_179-451,glycophorin_e_mrna,_complete_cds,glycophorin_e_mrna,_complete_cds
u13706_3-63,elav-like_neuronal_proteinisoform_hel-n2_(hel-
n1)_mrna,_partial_cds/gb=u13706_/ntype=rna

u14383_958-1372,mucin_(muc8)_mrna,_partial_cds_
 u20536_935-1428,cysteine_protease_mch2_isoform_alpha_(mch2)_mrna,_complete_cds_
 u33921_578-1046,_hsu33921cdna_
 u50535_1856-2270,brca2_region,_mrna_sequence_cg006_
5 u58970_1284-
 1824,putative_outer_mitochondrial_membrane_34_kda_translocase_htom34_mrna,_complete_cds
 u66406_2835-3255,putative_eph-related_ptk_receptor_ligand_lerk-8_(eplg8)_mrna,_complete_cds
 u90065_615-1178,potassium_channel_kcnol_mrna,_complete_cds_
 v00551mrna_366-878,_messenger_rna_forleukocyte_(alpha)_interferon
10 all_x05345_1772-1953,mrna_for_histidyl-trna_synthetase_(hrs)_
 x14448mrna_1017-1299:in_reversesequence,_11301-11319,gla_gene_for_alpha-d-
 galactosidase_a_(ec_3.2.1.
 x86012cds_61-319:in_fullsequence,_6603-
 6795,dna_sequence_from_intron_22_of_the_factor_viii_gene,_xq2
15 all_y00477_5141-
 5216,bone_marrow_serine_protease_gene_(medullasin)_leukocyte_neutrophil_elastase_ge

Metagene 173

20 m24736_3222-3785,endothelial_leukocyte_adhesion_molecule(elam-1)_mrna,_complete_cds_
 y07565cds_307-614:in_reversesequence,_833-1024,mrna_for_rin_protein_

Metagene 167

25 hg4704-ht5146_at_hg4704-ht5146_glial_growth_factor
 m19301mrna_944-1448,branched-chain_alpha-
 keto_acid_dehydrogenase_(e2)_mrna,_complete_cds_
 m95610_1971-2493,alphatype_ix_collagen_(col9a2)_mrna,_partial_cds_
 u65437mrna_7-307,homeodomain-containing_protein_(hanf)_gene,_partial_cds

30
Metagene 161

ab006781_528-1007,mrna_for_galectin-4,_complete_cds/gb=ab006781/_ntype=rna
 af007111_1609-2017,mdm2-like_p53-binding_protein_(mdmx)_mrna,_complete_cds
35 d49357_958-1438,mrna_for_s-adenosylmethionine_synthetase,_complete_cds_
 d86984_5659-6139,mrna_for_kiaa0231_gene,_partial_cds_
 hg2261-ht2351_s_at_hg2261-ht2351_antigen,_prostate_specific,_altslice_form_2
 hg3527-ht3721_f_at_hg3527-ht3721_luteinizing_hormone,_beta_subunit_
 hg3994-ht4264_at_hg3994-ht4264_cpg-enriched_dna,_clone_s16_

hg4058-ht4328_at_hg4058-ht4328_oncogene_aml1-evi-1,_fusion_activated_
 hg4533-ht4938_at_hg4533-ht4938_kallistatin,_protease_inhibitor_4_
 j04739mrna_1212-1650,bactericidal_permeability_increasing_protein_(bpi)_mrna,_complete_cds_
 115309_2444-2960,zinc_finger_protein_(znf141)_mrna,_complete_cds_
5 117075_1130-1607,tgf-b_superfamily_receptor_type_i_mrna,_complete_cds
 l24774_272-757,delta3,_delta2-coa-isomerase_mrna,_3'_end
 142583cds_1334-1665:in_reversesequence,_305-528,keratinisoform_k6a_(krt6a)_gene_
 all_m24900_1501-2054,triiodothyronine_recptor_(thra1,_ear1),_and_ear2_genes,_lastexons_each_
 m27093_2049-2509,nuclear-encoded_mitochondrial_branched_chain_alpha-
10 keto_acid_dehydrogenase_transacy
 m36067mrna_2602-3040,dna_ligase_i_mrna,_complete_cds_
 m73077_2770-3178,glucocorticoid_receptor_repression_factor(grf-1)_mrna,_complete_cds
 m94055_5925-6285,voltage-gated_sodium_channel_mrna,_complete_cds_
 all_u17894_870-1231,alpha(1,2)fucosyltransferase_(fut2)_gene,_complete_cds_
15 u38545_3056-3578,arf-activated_phosphatidylcholine-
 specific_phospholipase_d1a_(hp1d1)_mrna,_complete
 u45448_2014-2535,p2x1_receptor_mrna,_complete_cds
 u68727_2868-3414,homeobox-containing_protein_mrna,_complete_cds
 u90550_2991-3513,butyrophilin_(btf2)_mrna,_complete_cds
20 x76029cds_141-453:in_reversesequence,_636-756,mrna_for_neuromedin_u_
 all_x99226_4853-5412,mrna_for_faa_protein

Metagene 158

25 m92843_1144-1583,zinc_finger_transcriptional_regulator_mrna,_complete_cds
 u62015_1475-1841,cyr61_mrna,_complete_cds_
 v01512mrna#2_1533-2061,cellular_oncogene_c-fos_(complete_sequence)
 all_x51345_1604-1744,jun-b_mrna_for_jun-b_protein
 all_x52541_2549-3102,mrna_for_early_growth_response_protein(hegr1)
30 all_x68277_1459-1952,cl_100_mrna_for_protein_tyrosine_phosphatase
 all_x75918_2858-3417,mrna_for_not

Metagene 146

35 x12556mrna_3159-3483,mrna_for dbl_proto-oncogene_
 all_x52011_699-1144,myf6_gene_encoding_a_muscle_determination_factor_

Metagene 141

u19180_535-925,b_melanoma_antigen_(bage)_mrna,_complete_cds
 u30828_1078-1630,splicing_factor_srp55-2_(srp55)_mrna,_complete_cds
 u51269_3408-3900,armadillo_repeat_protein_mrna,_complete_cds_

5 Metagene 137

af005037_574-
 1030,secretory_carrier_membrane_protein_(scamp1)_mrna,_complete_cds/gb=af005037_/ntype=
 d87449_5359-5785,mrna_for_kiaa0260_gene,_partial_cds_
10 100972_2064-2202,cystathionine-beta-synthase_(cbs)_mrna
 149218exon_4-
 91,retinoblastoma_susceptibility_protein_(rb1)_e413kbp_deletion_mutant_(resulting_in_pr
 m88163_3059-3581,global_transcription_activator_homologous_sequence_mrna,_complete_cds_
 u79296_1366-1876,dihydrolipoamide_acetyl_transferase_mrna,_partial_cds.

15

Metagene 129

108010exon#6_94-211:not_in_gb_record,reg_gene_homologue,_complete_cds
 l32831exon_463-1036,g_protein-coupled_receptor_(gpr3)_gene,_complete_cds
20 m19888_58-580,small_proline_rich_protein_(spri)_mrna,_clone_128
 m19989_cds1_at_m19989_m19989,not_in_gb_record,platelet-
 derived_growth_factor_(pdgfa)_a_chain_gene,pl
 all_m59216_1586-2163:in_m59216cds_1091,gamma-aminobutyric_acid-a_(gaba-a)_receptor_beta-
 1_subunit_
25 u58681cds_807-1116:in_reversesequence,_1191-1434:not_in_gb_record,neurogenic_basic-helix-
 loop-helix_
 all_x63337_548-1101,hb2a_gene_for_high_sulfur_keratin
 z29572cds_52-322:in_reversesequence,_95-605,antisense_mrna_for_bcma_peptide
 z48511exon#4_572-1148,xg_mrna_(clone_pep11)

30

Metagene 88

d13640_4563-5091,mrna_for_kiaa0015_gene,_complete_cds
 hg2414-ht2510_s_at_hg2414-ht2510_prostaglandin_receptor_ep1_subtype
35 hg3236-ht3413_f_at_hg3236-ht3413_neurofibromatostumor_suppressor
 hg3342-ht3519_s_at_hg3342-ht3519_id1_
 j03801_911-1418,lysozyme_mrna,_complete_cds_with_an_alu_repeat_in_the_3'_flank_
 all_100389_1196-1792,cytochrome_p-450gene_
 m11058mrna_2351-2879,3-hydroxy-3-methylglutaryl_coenzyme_a_reductase_mrna,_complete_cds

m19045_907-1414,lysozyme_mrna,_complete_cds
 all_m31551_576-1134,urokinase_inhibitor_(pai-2)_gene_
 m31667_f_at_m31667_m31667_4040_in_all_m31667_1679-
 2265,cytochrome_p450_(cyp1a2)_gene_
5 u32576mrna_19-535,apolipoprotein_apoc-iv_(apoc4)_gene,_complete_cds_
 u33267_1613-2081,glycine_receptor_beta_subunit_(glrb)_mrna,_complete_cds_
 u50361_16-319,calcium,_calmodulin-
 dependent_protein_kinase_ii_delta_mrna,_partial_cds/gb=u50361_/nty
 u60269cds#2_171-429,endogenous_retrovirus_herv-
10 k(hml6)_proviral_clone_hml6.17_putative_polymerase_an
 u72507mrna_855-1341,40871_mrna_partial_sequence
 x14008mrna_926-1433,lysozyme_gene_(ec_3.2.1.17)_
 all_x51417_1050-1651,mrna_for_steroid_hormone_receptor_herr2_
 y10207mrna_61-475,mrna_for_cd171_protein/gb=y10207_/ntype=rna
15

Metagene 83

d90224_2791-3319,mrna_for_glycoprotein_34_(gp34)_
 hg415-ht415_at_hg415-ht415_lectin,_galactoside-binding,_soluble,_2_
20 k03204mrna_582-1130,prb1_locus_salivary_proline-rich_protein_mrna,_clone_cp3,_complete_cds_
 m14758mrna#1_4264-4561,p-glycoprotein_(mdrl)_mrna,_complete_cds
 m36653_1448-1663,2-oct_factor_mrna,_complete_cds_
 m64231mrna_1264-1624,spermidine_synthase_gene,_complete_cds_
 m64358exon_16-189,rhom-3_gene,_exon/gb=m64358_/ntype=dna/_annot=exon_
25 all_u67368_952-1411,multiple_exostosis(ext2)_gene_
 all_x16105_1077-1226,mrna_for_rd_protein,_rna-binding
 x58255mrna_2472-2862,flg-2_gene_for_fibroblast_growth_factor_receptor
 all_x67235_1087-1595,mrna_for_proline_rich_homeobox_(prh)_protein
 y10209mrna_79-331,mrna_for_cd30l_protein/gb=y10209_/ntype=rna
30 all_z70723_1812-2239,mrna_for_serum Aryldiakylphosphatase

Metagene 65

d29642_2294-2582,mrna_for_kiaa0053_gene,_complete_cds
35 hg1155-ht4822_at_hg1155-ht4822_colony-stimulating_factor_1,_macrophage,_altslice_3
 hg1996-ht2044_at_hg1996-ht2044_guanine_nucleotide-binding_protein_rap2,_ras-
 oncogene_related_
 hg243-ht243_s_at_hg243-ht243_lowe_oculocerebrorenal_syndrome_protein_
 hg2797-ht2905_at_hg2797-ht2905_clathrin,_light_polypeptide_altslice_1

hg4011-ht4804_s_at_hg4011-ht4804_dystrophin-associated_glycoprotein_50_kda_altslice_2
 hg4757-ht5207_s_at_hg4757-ht5207_oncogene_mll-af4_fusion_activated
 j00268gene_270-1415,insulin_gene_
 178440mrna_2089-2509,stat4_mrna,_complete_cds_

5 m10321mrna_5749-6321,von_willebrand_factor_mrna,_3'_end
 m34455_1427-1889,interferon-gamma-inducible_indoleamine_2,3'-
 dioxygenase_(ido)_mrna,_complete_cds_

m61827mrna_1289-1850,leukosialin_(cd43)_gene,_complete_cds
 m74542_1131-1611,aldehyde_dehydrogenase_type_iii_(aldhiii)_mrna,_complete_cds

10 all_u24683_219-474,anti-b_cell_autoantibody_igm_heavy_chain_variable_v-d-
 j_region_(vh4)_gene,_clone_

u34587_1545-2061,corticotropin-releasing_factor_receptormrna,_complete_cds
 u48861_1914-2430,betanicotinic_acetylcholine_receptor_subunit_mrna,_complete_cds
 u51096_1240-1720,homeobox_protein_cdx2_mrna,_complete_cds

15 all_u58675_25626-39844,_or17-
 228_gene_extracted_fromolfactory_receptor_gene_cluster_on_chromosome_17
 u64315_2269-2832,dna_repair_endonuclease_subunit_(xpf)_mrna,_complete_cds
 u81600_368-734,paired-like_homeodomain_protein_prx-2_mrna,_partial_cds.
 u82010mrna_2432-

20 2930,_homo_sapiensheme_a:_farnesyltransferase_(cox10)_gene_promoter_region_and
 x58399mrna_491-903,l2-9_transcript_of_unrearranged_immunoglobulin_v(h)5_pseudogene.
 x60003mrna_543-965,delta_creb_mrna_for_camp-responsive_element_(cre)_binding_protein
 all_x63359_2216-2781,ugt2bio_mrna_for_udp_glucuronosyltransferase
 x68985cds_482-656,mrna_for_hepatic_leukemia_factor_

25 x72882cds_19-103:in_reversesequence,_144-186,14a6ck_dna_sequence
 x74764cds_2202-2538:in_reversesequence,_2903-3041,mrna_for_receptor_protein_tyrosine_kinase_

x75342cds_1407-1767:in_reversesequence,_2095-2239,shb_mrna
 all_x84213_1094-1357,bak_mrna_for_bcl-2_homologue
 x89416cds_1386-1440:in_reversesequence,_1533-1932,mrna_for_protein_phosphatase_5_

30 x91911cds_321-711:in_reversesequence,_912-950,mrna_for_rtvp-1_protein_
 x97267mrna_321-861,lpap_gene
 all_x98085_4149-4642,mrna_for_tenascin-r_

all_x99664_723-1276,mrna_for_protein_containing_sh3_domain,_sh3gl3_

all_y00796_4559-5109,mrna_for_leukocyte-associated_molecule-1_alpha_subunit_(lfa-
35 1_alpha_subunit)

y08409cds_4-385:in_reversesequence,_431,spot14_gene_

y08639cds_837-1353:in_reversesequence,_1953-2001,mrna_for_transcription_factor_rzrbeta

y09216_214-736,mrna_for_protein_kinase,_dyrk2

all_z11697_1190-1701,mrna_for_hb15

z23115cds_197-677:in_reversesequence,_817-835,bcl-xl_mrna_
z67743cds_1792-2320:in_reversesequence,_2350,mrna_for_clc-7_chloride_channel_protein

Metagene 57

5

all_141913_305-502,retinoblastoma_susceptibility_protein_(rb1)_gene,_exon_26,_bases_174145-
174668_in
all_x75958_1683-2170,trkb_mrna_for_protein-tyrosine_kinase_

10 Metagene 41

hg2441-ht2537_s_at_hg2441-ht2537_retinoblastoma_protein,_mutated_
m16282cds_25-133:in_reversesequence,_283-
469,fragile_x_locus_m2cContaining_an_unidentified_open_rea
15 all_m17254_1366-1889,erg2_gene_encoding_erg2_protein,_complete_cds_
u84540mrna_1083-1341,dystrobrevin_isoform_dtn-
3_(dtn)_gene,_exon_11b_and_complete_cds/gb=u84540_nty
y10202mrna_169-529,mrna_for_cd207_protein/gb=y10202_ntype=rna_

20 Metagene 37

j04076mrna_2171-2651,early_growth_responseprotein_(egr2)_mrna,_complete_cds_
m31659mrna_1130-1640,gt mitochondrial_solute_carrier_protein_homologue_mrna,_complete_cds
all_x95677_1773-2368,mrna_for_argbpib_protein/gb=x95677_ntype=rna_

25

Metagene 29

d78014_4608-4998,mrna_for_dihydropyrimidinase_related_protein-3,_complete_cds
hg2614-ht2710_at_hg2614-ht2710_collagen,_type_viii,_alpha_1
30 m61906_2813-3326,p13-kinase_associated_p85_mrna_sequence_
u29953mrna_1150-1468,pigment_epithelium-derived_factor_gene,_complete_cds_
u40572_1105-1627,beta2-syntrophin_(snt_b2)_mrna,_complete_cds
u79294_831-1371,clone_23748_mrna,_complete_cds.
x15525mrna_1670-2084,lysosomal_acid_phosphatase_gene_(ec_3.1.3.2)_exon(and_joined_cds)_
35 all_x68742_2942-3423,mrna_for_integrin_alpha_subunit
x96719cds_86-398:in_reversesequence,_674-710,mrna_for_aicl_(activation-induced_c-type_lecchin)_

Metagene 25

af001294_285-735,ipl_(ipl)_mrna,_complete_cds.
 d16227_589-943,mrna_for_bdp-1_protein_(a_member_of_the_recoverin_family),_complete_cds_
 d50930_4876-5368,mrna_for_kiaa0140_gene,_complete_cds
 d78012_2289-2793,mrna_for_dihydropyrimidinase_related_protein-1,_complete_cds
5 d79985_3997-4393,mrna_for_kiaa0163_gene,_complete_cds
 d90359_5384-5912,ccg1_mrna_
 hg2566-ht4792_r_at_hg2566-ht4792_microtubule-associated_protein_tau,_altslice_3,_exon_8_
 j03930exon#11_638-1118,intestinal_alkaline_phosphatase_(alpi)_gene,_complete_cds
 j04469exon#9_11-173:not_in_gb_record,mitochondrial_creatine_kinase_(ckmt)_gene,_complete_cds
10 j05249_941-1409,replication_protein_a_32-kda_subunit_mrna,_complete_cds
 l14856cds_746-1100:in_reversesequence,_1324-1393,somatostatin_receptor_gene,_complete_cds_
 l18983mrna_3114-3588,tyrosine_phosphatase_(ia-2/ptp)_mrna,_complete_cds_
 l27479_797-1307,x123_mrna,_3'_end
 147345_2141-2609,elongin_a_mrna,_complete_cds_
15 m36430_321-753,transducin_beta-1_subunit_mrna,_3'_end
 m57732mrna_2643-
 3165_hepatic_nuclear_factor(tcfl)_mrna,_complete_cds,_clones_hcl10,_hcl12,_hcl17,_an
 reverse_m81780_4000-4487:in_m81780cds#3_175-
 296_smpd1_gene_(acid_sphingomyelinase)_extracted_fromac
20 m88468_1378-1906,mevalonate_kinase_mrna,_complete_cds_
 u01147mrna_4659-5211,guanine_nucleotide_regulatory_protein_(abr)_mrna,_complete_cds
 u09584_1382-1835,pl6_protein_(pl6)_mrna,_complete_cds
 u47742_7360-7810,monocytic_leukaemia_zinc_finger_protein_(moz)_mrna,_complete_cds
 u47928_2047-2491,protein_a_alternatively_spliced_form(a-2)_mrna,_complete_cds_
25 u53786_6024-6432:not_in_gb_record,envoplakin_(evpl)_mrna,_complete_cds

Metagene 7

j00207mrna#2_661-1075,_ifna_gene_(interferon_alpha-
30 a)_extracted_fromleukocyte_interferon_(leif)_alph
 j05016mrna_2252-
 2824,(clone_pa3)_protein_disulfide_isomerase_related_protein_(erp72)_mrna,_complete_
 l41268_f_at_l41268_l41268,_4040_in_l41268mrna_1043-1571,natural_killer-
 associated_transcript(nkat2)_
35 m31776cds_35-365,brain_natriuretic_protein_(bnp)_gene,_complete_cds
 u82311_39-112,unknown_protein_mrna,_partial_cds/gb=u82311_/ntype=rna_
 all_x06661_1817-2340,mrna_for_27-kda_calbindin_
 x13100cds_3130-3466:in_reversesequence,_3496-3592,mrna_fragment_for_myosin_heavy_chain
 x64994cds_642-912:in_reversesequence,_1279-1471,hgmp07i_gene_for_olfactory_receptor_

Metagene 6

hg1139-ht4910_at_hg1139-ht4910_fk506-binding_protein,_altslice_2
5 m14123cds#4_3521-3935,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123/_ntype=dna/_annot=cds,_pol_f
 m27396mrna_1389-1842,asparagine_synthetase_mrna,_complete_cds
 m89470_2855-3271,paired-box_protein_(pax2)_mrna,_complete_cds
 s73885_1537-2082,_ap-4=basic_helix-loop-helix_dna-
10 binding_protein_[human,_cervical_carcinoma,_hela_c
 u35005_764-1278,jnk1_beta2_protein_kinase_(jnk1b2)_mrna,_complete_cds
 u51333_2437-3005,hexokinase_iii_(hk3)_mrna,_complete_cds_
 u73738_74-107,calcium/calmodulin-
 dependent_protein_kinase_ii_delta_e_mrna,_partial_cds/gb=u73738/_nt
15

Metagene 44

hg3733-ht4003_at_hg3733-ht4003_epiligrin,_alpha_3
 m65291_715-1189,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds,_clone_p35
20 u15422cds#2_17-269:in_reversesequence,_20347-
 20563,_prm2_gene_(protamine_2)_extracted_fromprotamine(
 u18297_1298-1805,mst1_(mst1)_mrna,_complete_cds

Metagene 461

25
 hg4340-ht4610_at_hg4340-ht4610_soxa
 u63332_3-361,super_cysteine_rich_protein_mrna,_partial_cds.
 u77413_2543-2975,o-linked_glcNAc_transferase_mrna,_complete_cds/gb=u77413/_ntype=rna_
 x97675mrna_3636-4212,_plakophilin_2a_gene_extracted_frommrna_for_plakophilin_2a_and_b_
30 all_z80781_583-748,h2b/j_gene

Metagene 418

hg458-ht458_f_at_hg458-ht458_beta-1-glycoprotein_1,_pregnancy-specific_
35 m22324_2954-3416,aminopeptidase_n/cd13_mrna_encoding_aminopeptidase_n,_complete_cds
 u04343_815-1361,cd86_antigen_mrna,_complete_cds
 u20760_4534-4966,extracellular_calcium-sensing_receptor_mrna,_complete_cds_
 u67849_25-187,beta-galactoside_alpha2,6-
 sialyltransferase_(sialt1)_mrna,_exon_w/gb=u67849/_ntype=rna

x59372mrna_610-1090,hox4c_mrna_for_a_homeobox_protein
x65614cds_10-262:in_reversesequence,_19-391,mrna_for_calcium-binding_protein_s100p_
x81892cds_2760-2994:in_reversesequence,_3126-3204,mrna_for_he6_tm7_receptor_
all_x95525_2560-3071,mrna_for_tafii100_protein_

5

Metagene 413

all_u03877_2037-2512,extracellular_protein_(s1-5)_mrna,_complete_cds_

10 Metagene 329

m27968mrna_3289-3658,basic_fibroblast_growth_factor_(fgf)_mrna,_complete_cds_
all_m31994_117-538,cytosolic_aldehyde_dehydrogenase_(aldh1)_gene_
m73780_3266-3746,integrin_beta-8_subunit_mrna,_complete_cds
15 u20860exon#3_1889-2279,angiotensin_ii_typtereceptor_gene,_complete_cds_
u65002_6724-7240,zinc_finger_protein_plagl1_mrna,_complete_cds
all_x04688_227-798,mrna_for_t-cell_replacing_factor_(interleukin-5)

Metagene 317

20

j03242_1155-1324,insulin-like_growth_factor_ii_mrna,_complete_cds_
j05068_984-1494,trancobalamin_i_mrna,_complete_cds
m32578_1131-1191,mhc_ii_hla-dr_beta-1_mrna_(dr2.3),_5'_end_
all_x79981_3411-3946,ve-cadherin_mrna

25

Metagene 271

m10901mrna_4325-4655,glucocorticoid_receptor_alpha_mrna,_complete_cds
m88338_1465-1867,serum_constituent_protein_(mse55)_mrna,_complete_cds
30 u03891_90-576,phorbolin_i_mrna,_partial_cds
u77643_1462-1972,k12_protein_precursor_mrna,_complete_cds
x74795cds_1923-2181:in_reversesequence,_2272-2488,p1-cdc46_mrna_
all_x78669_1114-1643,erc-55_mrna_

35 Metagene 245

y09912mrna_757-1315,ap-2_beta_gene

Metagene 185

af009301_2752-3262,teb4_protein_mrna,_complete_cds/gb=af009301/_ntype=rna
 u73304mrna_4973-5447,cb1_cannabinoid_receptor_(cnr1)_gene,_complete_cds.
 x53414mrna_907-1453,mrna_for_peroxisomal_l-alanine:glyoxylate_aminotransferase_
5 x59739mrna_5061-5473,zfx_mrna_for_puttranscription_activator,_isoform_2
 x60955cds_2-147:in_reversesequence,_154-168,tyrrp_gene_for_tyrosinase-related_protein_(trp-
 1)_(parti)

Metagene 163

10
 d63882_1015-1568,hslim15_mrna_for_hslim15,_complete_cds
 hg2188-ht2258_at_hg2188-ht2258_paired_box_hup1_
 m37825_624-1044,fibroblast_growth_factor-5_(fgf-5)_mrna,_complete_cds
 m60092mrna_1743-2295,myoadenylate_deaminase_(ampd1)_mrna,_complete_cds_
15 s67798_1420-1930,_ph-20_[human,_testis,_mrna,_1973_nt]
 u49065_1400-1922,interleukin-1_receptor-
 related_protein_mrna,_complete_cds/gb=u49065/_ntype=rna
 u82671mrna#2_1536-1776:in_reversesequence,_106561-106657,_hsp1-
 a_gene_extracted_fromcosmids_qc14e2,_
20 all_u83303_1160-2035,_gcp-2_gene_(granulocyte_chemotactic_protein-2)_extracted_fromline-
 1_reverse_tr'
 all_x91148_3331-3824,mrna_for_microsomal_triglyceride_transfer_protein_

Metagene 103

25
 u59877_295-750,low-mr_gtp-binding_protein_(rab31)_mrna,_complete_cds_
 x51441cds_28-
 65:in_reversesequence,_228,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clone_pas3-a
 all_x52075_5011-5273,gene_for_sialophorin_(cd43)
30 all_z11559_2897-3480,mrna_for_iron_regulatory_factor_
 all_z29331_1560-1981,(23k/3)_mrna_for_ubiquitin-conjugating_enzyme_ubch2_

Metagene 80

35
 hg2479-ht2575_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
 m55682cds_1132-1467:in_reversesequence,_439-571,cartilage_matrix_protein_(cmp)_gene_
 s77583_4-
 66,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt244}_*[human,_multiple_sclerosis,_

Metagene 55

d13626_1857-2373,mrna_for_kiaa0001_gene,_complete_cds

5

Metagene 417

hg3299-ht3476_at_hg3299-ht3476_acetyl-coenzyme_a_carboxylase_

u79265_1269-1623,clone_23614_mrna_sequence_

10 x12901cds_2080-2431:in_reversesequence,_2551-2629,mrna_for_villin_

Metagene 287

d17525mrna_3966-4446,mrna_for_precursor_of_p100_serine_protease_of_ra-

15 reactive_factor,_complete_cds

d28483_944-1466,scr3_mrna_for_rna_binding_protein_scr3,_complete_cds_

d28532_1223-1763,mrna_for_renal_na+-dependent_phosphate_cotransporter,_complete_cds

d31628cds_781-1132,gene_for_4-hydroxyphenylpyruvic_acid_dioxygenase_(hpd),_comlete_cds_

hg2707-ht2803_at_hg2707-ht2803_serine/threonine_kinase_

20 j04990cds_371-683:in_reversesequence,_2929-2989,cathepsin_g_gene,_complete_cds

j05257_1239-1713,(clones_mdp4,_mdp7)_microsomal_dipeptidase_(mdp)_mrna,_complete_cds

102321_1089-1509,glutathione_s-transferase_(gstm5)_mrna,_complete_cds

l08485_1759-2257,gaba-benzodiazepine_receptor_alpha-5-subunit_(gabra5)_mrna,_complete_cds

m34065mrna_1526-1952,cdc25hs_mrna,_complete_cds

25 s68287_662-1124,_chlordecone_reductase_{clone_hakra}_[_human,_liver,_mrna,_1167_nt]

u64863_1556-2030,hpd-1_(hpd-1)_mrna,_complete_cds

Metagene 225

30 d21205_1715-2279,mrna_for_estrogen_responsive_finger_protein,_complete_cds_

hg2271-ht2367_s_at_hg2271-ht2367_profilaggrin

hg2981-ht3125_s_at_hg2981-ht3125_epican,_altssplice_1_

117330_88-586,pre-t/nk_cell_associated_protein_(6h9a)_mrna,_complete_cds_

176927mrna_760-1330,galactokinase_(galk1)_gene,_complete_cds

35 m31520mrna_2-

131,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna_

u52111mrna#3_2176-

2659,xq28_genomic_dna_in_the_region_of_the_ald_locusContaining_the_genes_for_crea

u57317_2551-2989,p300/cbp-associated_factor_(p/caf)_mrna,_complete_cds_

u66468_586-1126,cell_growth_regulator_cgr11_mrna,_complete_cds_

Metagene 169

- 5 d50928_2629-3019,mrna_for_kiaa0138_gene,_complete_cds
hg2417-ht2513_at_hg2417-ht2513_dynein,_heavy_chain,_cytoplasmic
m15958cds_12-282:in_reversesequence,_6718-6778,gastrin_gene,_complete_cds_
u68162mrna_3059-
3585,_mpl_gene_(thrombopoietin_receptor)_extracted_fromthrombopoietin_receptor_(mpl)
- 10 all_x60484_683-858,h4/e_gene_for_h4_histone
x68505_2403-2879,mrna_for_myocyte-specific_enhancer_factor(mef2)

Metagene 132

- 15 d37781_4150-4705,mrna_for_protein-tyrosine_phosphatase_hptpeta,_complete_cds_
j00209mrna_366-878,leukocyte_interferon_(ifn-alpha)_alpha-c_mrna,complete_cds
m90696_1168-1738,cathepsin_s_(ctss)_mrna,_complete_cds_
u03735exon#3_970-1517,mage-3_antigen_(mage-3)_gene,_complete_cds_

20 Metagene 105

- u38276_2969-3509,semaphorin_iii_family_homolog_mrna,_complete_cds
all_x17093_3834-4023,hla-f_gene_forleukocyte_antigen_f
all_x59798_3705-4192,prad1_mrna_for_cyclin_

25

Metagene 104

- d78611_1893-2331,mest_mrna,_complete_cds_
l01406_1010-1562,growth_hormone-releasing_hormone_receptor_mrna,_complete_cds
- 30 m20919cds_478-568:in_reversesequence,_899-
927,dna_with_a_hepatitis_b_virus_surface_antigen_(hbsag)_g

Metagene 24

- 35 l34357_1655-2165,gata-4_mrna,_complete_cds
u09860_3095-3653,enterokinase_mrna,_complete_cds_
u33448cds_773-1108:in_reversesequence,_1666-1883,putative_g-protein-coupled_receptor_(gpr16)_gene,_c
u40370_1443-1929,3'_5'_cyclic_nucleotide_phosphodiesterase_(hspde1a3a)_mrna,_complete_cds_

all_x02750_1332-1729,liver_mrna_for_protein_c
z47727cds_6-150:in_reversesequence,_28-313,mrna_for_rna_polymerase_ii_subunit
z80780cds_2-339,h2b/h_gene.

5 Metagene 366

ad000092cds#7_730-1062:in_reversesequence,_99587-99822,_hypotheticalserine-threonine_protein_kinase_
d50405_1628-2054,mrna_for_rpd3_protein,_complete_cds_
10 d50925_3408-3918,mrna_for_kiaa0135_gene,_partial_cds_
d87442_2204-2684,mrna_for_kiaa0253_gene,_partial_cds_
104490_954-1362,(clone_cc6)_nadhh-ubiquinone_oxidoreductase_subunit_mrna,_3'_end_cds_
l37033_1039-1480,fk-506_binding_protein_homologue_(fkbp38)_mrna,_complete_cds
m92269cds_6175-6626:in_reversesequence,_6958-7053,1-
15 type_calcium_channel_hfcc_mrna,_complete_cds
u94585_1810-2308,requiem_homolog_(hsreq)_mrna,_complete_cds.
all_x02596_4186-
4733,mrna_for_bcr_(breakpoint_cluster_region)_gene_in_philadelphia_chromosome
all_x69550_1266-1801,mrna_for_rho_gdp-dissociation_inhibitor_1_
20 x80200_1428-1866,mln62_mrna
all_x80497_3995-4428,phkla_mrna
z21488cds_2749-3016:in_reversesequence,_3179-3326,contactin_mrna
all_z48054_2544-3067,mrna_for_peroxisomal_targeting_signal(skl_type)_receptor_-

25 Metagene 121

d00749exon_346-525,t_cell_surface_antigen_cd7_gene_
hg1877-ht1917_s_at_hg1877-ht1917_myelin_basic_protein,_altslice_form_4
hg4126-ht4396_at_hg4126-ht4396_zinc_finger_protein_hzf4
30 m97287_2345-2885,mar/sar_dna_binding_protein_(satb1)_mrna,_complete_cds
x98178cds_567-607,mrna_for_mach-beta-4_protein/gb=x98178_/ntype=mrna
y07755exon#2-3_16-204,s100a2_gene,_exon_1, and _3_
z30426_at_z30426_z30426,not_in_gb_record,gene_for_early_lymphocyte_activation_antigen_cd69,
_exon_1

35

Metagene 49

hg4316-ht4586_at_hg4316-ht4586_transketolase-like_protein

Metagene 382

hg4458-ht4727_at_hg4458-ht4727_immunoglobulin_heavy_chain_vdj_c_regions
 all_100058_470-855,(gh)_germline_c-myc_proto-oncogene,_5'_flank
5 u16258_1212-1776,i_kappa_br_mrna,_complete_cds_
 all_x82629_1744-2297,mrna_for_mox-2
 x97324cds_749-1277,mrna_for_adipophilin/gb=x97324_ntype=rna_

Metagene 365

10 ad001527cds#1_317-575:in_reversesequence,_3640-3802,_comment_for_location_3447-
 3655:_blastx_gi|10329
 m31423cds_322-640:in_reversesequence,_1200-1320,cerebellar-degeneration-
 related_antigen_(cdr34)_gene
15 u44060_2395-2845,homeodomain_protein_(prox_1)_mrna,_complete_cds_
 u57093_501-969,small_gtp-binding_protein_rab27b_mrna,_complete_cds_

Metagene 281

20 d28235exon#10_1923-2282,ptgs2_gene_for_prostaglandin_endoperoxide_synthase-
 2,_complete_cds_
 all_k02545_752-1044,_tcrb_gene_extracted_fromt-cell_receptor_germline_beta-chain_j-beta-
 1_gene_clust
 all_x98330_15142-15731,mrna_for_ryanodine_receptor_2_

25

Metagene 180

m21188mrna_2754-3204,insulin-degrading_enzyme_(ide)_mrna,_complete_cds_
 s66896_1272-
30 1638_squamous_cell_carcinoma_antigen=serine_protease_inhibitor_[human,_mrna,_1711_nt]
 u06452_923-1475,melanoma_antigen_recognized_by_t-cells_(mart-1)_mrna_
 u13616_14235-14709,ankyrin_g_(ank-3)_mrna,_complete_cds
 all_x70340_3545-4062,mrna_for_transforming_growth_factor_alpha_

35 Metagene 155

m26683_416-510,interferon_gamma_treatment_inducible_mrna_
 m60314_1582-2044,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_
 u02310_2946-3372,fork_head_domain_protein_(fKHR)_mrna,_complete_cds

u57796_3322-3784,zinc_finger_protein_(ld5-1)_mrna,_complete_cds
 all_u60116_905-966:not_in_gb_record,skeletal_muscle_lim-protein_slim2_mrna,_partial_cds_

Metagene 79

5

u00802_1922-2463,drebrin_e2_mrna_(dbn1),_complete_cds
 u77594_245-599,tazarotene-induced_gene(tig2)_mrna,_complete_cds_
 u86136_8094-8472,telomerase-associated_protein_tp-1_mrna,_complete_cds_
 x82494mrna_3527-3965,mrna_for_fibulin-2

10

Metagene 186

m11726exon#1_49-163:in_reversesequence,_1559-
15 2534:not_in_gb_record,pancreatic_polypeptide_gene,_comp
 u15590_306-840,heat_shock_protein_27_(hsp27)_mrna,_complete_cds

Metagene 166

20 af001359_2-
 27,dna_mismatch_repair_protein_(hmlh1)_mrna,_alternatively_spliced,_partial_cds/gb=af0013
 hg627-ht5097_s_at_hg627-ht5097_rhesus_(rh)_blood_group_system_ce-antigen,_alts splice_2,_rhvi
 hg627-ht5098_s_at_hg627-ht5098_rhesus_(rh)_blood_group_system_ce-
 antigen1,_alts splice_3,_rhviii_
25 105144_2488-2598,(clone_lamda-hpec-
 3)_phosphoenolpyruvate_carboxykinase_(pck1)_mrna,_complete_cds_
 all_105187_2284-2339,small_proline-rich_protein(sprrla)_gene,_complete_cds_
 118877exon#2_980-1530,mage-12_protein_gene,_complete_cds_
 120469_499-996,truncated_dopamine_d3_receptor_mrna,_complete_cds.
30 m23323mrna_779-1309,membrane_protein_(cd3-epsilon)_gene
 s72503_1692-
 1870,_hrk1=inward_rectifier_potassium_channel_[human,_hippocampus,_mrna,_1913_nt]
 u12707_1280-1744,wiskott-aldrich_syndrome_protein_(wasp)_mrna,_complete_cds
 u15641_760-1283,transcription_factor_e2f-4_mrna,_complete_cds
35 u20979_2612-3068,chromatin_assembly_factor-i_p150_subunit_mrna,_complete_cds_
 u73167cds#2_79-
 834,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted_fromcos
 x87344mrna#26_769-945,dma,_dmb,_hla-
 z1,_ipp2,_imp2,_tap1,_imp7,_tap2,_dob,_dqb2_and_ring8,_9, and gene

x97064cds_1988-2210:in_reversesequence,_2435-2678,mrna_for_sec23a_isoform,_2748bp
 z30644cds_1860-1918:in_reversesequence,_2130-
 2138,mrna_for_chloride_channel_(putative)_2163bp_

5 Metagene 34

hg3992-ht4262_at_hg3992-ht4262_cpg-enriched_dna_clone_e35_
 j02843cds_1103-1451:in_reversesequence,_14089-14119,cytochrome_p450iie1_(ethanol-inducible)_gene,_co
10 m54927mrna_2349-2907,myelin_proteolipid_protein_mrna,_complete_cds_
 u38480_1008-1521,retinoid_x_receptor-gamma_mrna,_complete_cds
 x05608exon#4_172-406:not_in_gb_record,gene_for_neurofilament_subunit_nf-1_

Metagene 22

15 af001787_990-1150,uncoupling_proteinmrna,_complete_cds/gb=af001787_/ntype=rna
 s81957mrna#1_40-112,_bmp-5=bone_morphogenic_protein-
 5_{promoter}_{[human,_genomic,_1116_nt]}/gb=s81957
 all_x55777_1833-
20 2326,_putorf_gene_extracted_frommahlavu_hepatocellular_carcinoma_hhc(m)_dna_

Metagene 323

149229cds_2-
25 87,retinoblastoma_susceptibility_protein_(rb1)_gene,_with_abp_deletion_in_exon_22_(11191
 y09305cds_267-675:in_reversesequence,_711-771,mrna_for_protein_kinase,_dyrk4,_partial_
 y10517mrna_252-606,mrna_for_cd108_protein/gb=y10517_/ntype=rna_

Metagene 266

30 u18467_1436-1946,pregnancy-specific_beta_1-glycoprotein(psg7)_mrna,_complete_cds
 u65918_1248-1820,putative_rna_binding_protein_(dazh)_mrna,_complete_cds
 z78290_44-109,mrna_(clone_1d7).

35 Metagene 94

u66581cds_963-1275:in_reversesequence,_1547-1745,putative_g_protein-coupled_receptor_(gpr22)_gene,_c
 u73799_34-265,dynactin_mrna,_partial_cds/gb=u73799_/ntype=rna

u88892_31-241,tenascin-c_mrna,_splice_variant_tncfn-ad2,_partial_cds/gb=u88892_/ntype=rna
 all_x73501_11784-13955,gene_for_cytokeratin_20_
 x97249cds_1720-2230,mrna_for_leucine-rich_primary_response_protein_1_
 all_x97261_25-333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
5 all_z32684_4621-5042,xk_mrna_for_membrane_transport_protein

Metagene 285

d37931_395-911,mrna_for_rnase_4,_complete_cds
10 hg3731-ht4001_at_hg3731-ht4001_immunoglobulin_heavy_chain,_vdjrc_regions_
 hg4668-ht5083_s_at_hg4668-ht5083_transcription_factor_mef2,_altslice_2
 l23333_725-1305,corticotropin_releasing_factor_receptor_mrna,_complete_cds.
 l38503_531-993,glutathione_s-transferase_theta(gstt2)_mrna,_complete_cds_
 m13981_1253-1300,inhibin_a-subunit_mrna,_complete_cds
15 all_m35093_2155-2456,secreted_epithelial_tumor_mucin_antigen_(muc1)_gene,_complete_cds_
 u15932_1928-2294,dual-specificity_protein_phosphatase_mrna,_complete_cds_
 u79249_873-1359,clone_23839_mrna_sequence
 x65727cds#1_199-591,_gstalpha_locus_gene_(glutathione_s-
 transferase)_extracted_fromgstalpha_gene_for
20 all_x77166_798-1183,gene_for_kunitz-type_protease_inhibitor,_hkib9_
 x95097mrna_924-1503,mrna_for_vip2_receptor
 all_z46261_490-899,dna_for_histone_h3a

Metagene 367

25
 hg4236-ht4506_f_at_hg4236-ht4506_zinc_finger_protein_znf138
 l32606_1862-2196,homeobox-like_mrna
 m61826exon_72-568,alpha-spectrin_gene
 u09279_1375-1777,type_xix_collagen_(col19a1)_mrna,_partial_cds_
30 u38964cds_1096-1146,in_reversesequence,_1291-
 1359,pms2_related_(hpmsr2)_gene,_complete_cds_
 u79301_999-1509,clone_23842_mrna_sequence
 x00540_at_x00540_x00540,not_in_gb_record,gene_encoding_prolactin,_exonand_joined_cds_
 all_x15088_1146-1276,gnat1_mrna_for_transducin_alpha-chain_
35

Metagene 269

hg3985-ht4255_at_hg3985-ht4255_cpg-enriched_dna,_clone_e04_
 m16967_6338-6806,coagulation_factor_v_mrna,_complete_cds_

m59941_2557-2965,gm-csf_receptor_beta_chain_mrna,_complete_cds_
 u00672_3067-3577,interleukin-10_receptor_mrna,_complete_cds
 u79526_1787-2327,orphan_g-protein_coupled_receptor_dez_isoform_a_mrna,_complete_cds
 reverse_z49208_20545-
5 20696,dna_from_cosmid_1161a8,_huntington_disease_region,_chromosome_4p16.3

Metagene 30

j04132_919-1417,t_cell_receptor_zeta-chain_mrna,_complete_cds
10 m76559_3065-3521,neuronal_dhp-sensitive,_voltage-dependent,_calcium_channel_alpha-
 2b_subunit_mrna,_c
 m81882mrna_1835-2261,glutamate_decarboxylase_(gad65)_mrna,_complete_cds
 s68874_113-469,_ep3_prostanoid_receptor_ep3-
 i_{3'_region,_alternatively_spliced}_[_human,_mrna_partia
15 u00921exon#3_273-313:not_in_gb_record,lst-1_gene,_complete_cds
 u01828_5837-5942,microtubule-associated_protein(map2)_mrna,_complete_cds
 u20759_3683-3758,parathyroid_cell_calcium-sensing_receptor_mrna,_complete_cds
 u29943_1609-2065,elav-like_neuronal_protein-2_hel-n2_mrna,_complete_cds
 u31628_1015-1507,interleukin-15_receptor_alpha_chain_precursor_(il15ra)_mrna,_complete_cds_-
20 x02883exon#4_568-736,gene_for_t-
 cell_receptor_alpha_chain_c_region/gb=x02883_/ntype=dna/_annot=exon
 all_x70811_2067-2566,mrna_for_betaadrenergic_receptor_-
 all_x81832_1592-2163,mrna_for_glucose-dependant_insulinotropic_polypeptide_receptor_gene_-
 x86570_1208-1532,mrna_for_acidic_hair_keratin_1
25 y07683_951-1413,mrna_for_p2x3_purinoceptor/gb=y07683_/ntype=rna

Metagene 115

all_m16441_2260-
30 2855,_lymphotoxin_gene_extracted_fromtumor_necrosis_factor_and_lymphotoxin_genes,_co

Metagene 23

all_x77748_2815-3296,mrna_for_metabotropic glutamate_receptor_type_3_-
35 x84003cds_140-305:in_reversesequence,_373-379,tafii18_mrna_for_transcription_factor_tfid_-
 y10510mrna_13-268,mrna_for_cd67s_protein/gb=y10510_/ntype=rna

Metagene 405

ab000381exon#2-4_45-395:not_in_gb_record,dna_for_gpi-anchored_molecule-like_protein,_complete_cds_
 all_d16154_2725-2751:not_in_gb_record,gene_for_cytochrome_p-450c11,_exon_3-9/gb=d16154_/ntype=dna/_a
5 j02982_23-439,glycophorin_b_mrna,_complete_cds_
 110373_1311-1713,(clone_ccg-b7)_mrna_sequence
 121893_1039-1537,na/taurocholate_cotransporting_polypeptide_mrna,_complete_cds_
 m13928mrna_542-1020,delta-aminolevulinate_dehydratase_mrna,_complete_cds.
 all_m29037_3259-3548,_humanbeta-hydroxysteroid_dehydrogenase_(17bhsdi)_gene,_exons_1-
10 5,_complete_cds
 s78825_523-667,_id1_(id1-b)=transcription_regulator_helix-loop-helix_protein_{alternatively_spliced}
 u12424_2016-2564,mitochondrial_glycerol-3-phosphate_dehydrogenase_mrna,_complete_cds_
 u61276_4243-4777,transmembrane_protein_jagged(hj1)_mrna,_complete_cds_
15 all_u83598_780-
 815,death_domain_receptorsoluble_form_(ddr3)_mrna,_partial_cds,death_domain_receptors
 v01510mrna_506-
 1022,_pomc_gene_(proopiomelanocortin)_extracted_fromgene_coding_for_acth_and_beta-lph
 x92493mrna_2160-2672,mrna_for_stm-7_protein
20 y10511mrna_16-343,mrna_for_cd176_protein/gb=y10511_/ntype=rna

Metagene 4

ac002477cds_444-988,pac_clone_dj327a19_from_xq25-q26,_complete_sequence/gb=ac002477_/ntype=dna/_anno
 hg4243-ht4513_at_hg4243-ht4513_zinc_finger_protein_znf155
 j00129mrna#1_1282-1552:not_in_gb_record,fibrinogen_beta-chain_mrna,_partial_cds_
 all_m58026_831-1240,nb-1_mrna,_complete_cds
 u30255_977-1493,phosphogluconate_dehydrogenase_(hpgdh)_gene,_complete_cds
25 u37022mrna_860-1322,cyclin-dependent_kinase(cdk4)_gene,_complete_cds_
 u67191_3391-3967,multiple_exostosis-like_protein_(extl)_mrna,_complete_cds_
 u67369_2300-2720,growth_factor_independence-1_(gfi-1)_mrna,_complete_cds_
 u85245_3310-3718,phosphatidylinositol-4-phosphate_5-kinase_type_ii_beta_mrna,_complete_cds.
 u97018_3439-3853,echinoderm_microtubule-associated_protein_homolog_huemap_mrna,_complete_cds
30 x13461cds_88-422:in_reversesequence,_1502-1737,intronless_calmodulin-like_gene_(clp_gene)_for_calmod
 all_x72632_1746-2326,mrna_encoding_rev-erbaalpha_(internal_fragment).
 z48314cds_2683-3086:in_reversesequence,_3110-3249,mrna_for_apomucin_

Metagene 410

d17547_2106-2262,mrna_for_dopachrome_tautomerase_(tyrosinase-related_protein-
 5 2),_complete_cds
 k02054mrna_238-676,gastrin-releasing_peptide_mrna,_complete_cds
 l33404_464-890,stratum_corneum_chymotryptic_enzyme_mrna,_complete_cds
 m64108_2031-2571,udulinmrna,_3'_end_
 s83198_412-916,_bpplp=basic_proline-rich_protein_[human,_lacrimal_gland,_mrna,_947_nt]
 10 u60206_1537-2003,stress_responsive_serine/threonine_protein_kinase_krs-1_mrna,_complete_cds
 u73960_566-1022,adp-ribosylation_factor-like_proteinmrna,_complete_cds

Metagene 398

15 hg2507-ht2603_at_hg2507-ht2603_potassium_channel,_voltage-gated_konc1
 j03258mrna_4003-4561,vitamin_d_receptor_mrna,_complete_cds_
 k02268mrna_3155-3677,enkephalin_b_(enkfb)_gene,_5'_flank_and
 105606_1219-1741,myosin_binding_protein_h_mrna,_complete_cds_
 l12392_9795-10257,huntington_disease_(hd)_mrna,_complete_cds
 20 l15533mrna_236-764,pancreatitis-associated_protein_(pap)_gene,_complete_cds_
 l76380mrna_2459-2969,(clone_hsnme29)_cgrp_typrereceptor_mrna,_complete_cds
 all_m16424_135-664,beta-hexosaminidase_alpha_chain_(hexa)_gene_
 s78296_2596-3076,_neurofilament-66_[human,_fetal_brain,_mrna,_3197_nt]
 u57092_317-779,small_gtp-binding_protein_rab30_
 25 u76369_13-325,cationic_amino_acid_transporter-
 2b_(atrc2)_mrna,_partial_cds/gb=u76369_/ntype=rna
 x52425mrna_3032-3536,il-4-r_mrna_for_the_interleukinreceptor

Metagene 309

30 d88146_1156-1408,mrna_for_udp-galactose_transporter_2,_complete_cds
 hg2175-ht2245_s_at_hg2175-ht2245_myosin,_heavy_polypeptide_10,_non-muscle
 hg3991-ht4261_at_hg3991-ht4261_cpg-enriched_dna,_clone_e18_
 all_m19989_804-1279,platelet-derived_growth_factor_(pdgfa)_a_chain_gene,platelet-
 35 derived_growth_fact
 u30313_372-756,diadenosine_tetraphosphatase_mrna,_complete_cds/gb=u30313_/ntype=rna
 u66077_1401-1822,daz_mrna,_3'_utr
 u79272_699-1179,clone_23720_mrna_sequence

x98337cds_643-971:in_reversesequence,_1061-1256,mrna_for_complement_factor_h-related_protein_4

Metagene 214

5

d26135_3247-3619,mrna_for_diacylglycerol_kinase_gamma,_complete_cds
hg3105-ht3281_s_at_hg3105-ht3281_atpase,_cu2+_transporting
s78774_411-717,_na+/ca2+_exchanger_[human,_neuroblastoma_x_glioma_hybrid_ng108-15_cells,_mrna_partia

10 x98225cds_31-331,mrna_for_gastrin-binding_protein/gb=x98225_/ntype=rna

Metagene 38

d21267mrna_1481-1979,mrna_for_highly_expressed_protein_
15 d83781_4231-4729,mrna_for_kiaa0197_gene,_partial_cds_
hg3930-ht4200_at_hg3930-ht4200_stearoyl-coenzyme_a_desaturase_
142176_844-1384,(clone_35.3)_dral_mrna,_complete_cds
149054_587-1067,t(3;5)(q25.1;p34)_fusion_gene_npm-mlf1_mrna,_complete_cds.
m95167mrna_3333-3897,dopamine_transporter_(slc6a3)_mrna,_complete_cds_
20 u32376_2548-3028,channel_associated_protein_of_synapse_(chapsyn-110)_mrna,_complete_cds
x78712cds_1319-1637:in_reversesequence,_1691-1823,mrna_for_glycerol_kinase_testis_specific_2
x82209_7019-7511,mn1_mrna
y10505mrna_94-658,mrna_for_cd104_protein/gb=y10505_/ntype=rna

25 Metagene 456

u30246_3599-4019,bumetanide-sensitive_na-k-cl_cotransporter_(nkcc1)_mrna,_complete_cds_

Metagene 153

30

hg4245-ht4515_at_hg4245-ht4515_forkhead_family_afx1
m84349mrna_1366-1852,transmembrane_protein_(cd59)_gene_

Metagene 422

35

d14678_1244-1748,mrna_for_kinesin-related_protein,_partial_cds_
d31833_1212-1768,mrna_for_vasopressin_v1b_receptor,_complete_cds_
d86043_1741-1829,mrna_for_shps-1,_complete_cds_
l03427_4325-4844,zinc_finger_protein_basonuclin_mrna,_complete_cds_

115344_1360-1768,high_molecular_weight_b_cell_growth_factor_mrna_sequence
 m85165_1311-1809,srf_accessory_protein_1a_(sap-1)_mrna,_complete_cds
 m95936_1148-1466,protein-serine/threonine_(akt2)_mrna,_complete_cds
 s78271_4580-5111,_sb1.8/dxs423e=mitosis-
5 specific_chromosome_segregation_protein_smc1_homolog_[human,
 u03905_1438-1858,monocyte_chemoattractant_proteinreceptor_(mcp-
 1rb)_alternatively_spliced_mrna,_comp
 u09002_5527-6082,n-methyl-d-
 aspartate_receptor_modulatory_subunit_2a_(hnr2a)_mrna,_complete_cds
10 u13395_994-1450,oxidoreductase_(hhcma56)_mrna,_complete_cds
 u28281_1162-1618,secretin_receptor_mrna,_complete_cds
 u50531_4295-4847,brca2_region,_mrna_sequence_cg030_
 u66618_1518-2016,swi/snf_complex_60_kda_subunit_(baf60b)_mrna,_complete_cds
 u85767_13-505,myeloid_progenitor_inhibitory_factor-1_mpif-1_mrna,_complete_cds_
15 x14767mrna_1685-1832,mrna_for_gaba-a_receptor,_betasubunit

Metagene 272

m86917_2402-2972,oxysterol-binding_protein_(osbp)_mrna,_complete_cds_
20 u19142_69-510,gage-1_protein_mrna,_complete_cds
 u30872_9600-10116,mitosin_mrna,_complete_cds_
 all_u66061_134531-176445,germline_t-
 cell_receptor_beta_chain_tcrbv17s1alt,_tcrbv2s1,_tcrbv10s1p,_tcr
 u79297_1095-1575,clone_23589_mrna_sequence_
25 u90268_1427-1703,krit1_mrna,_complete_cds
 all_x07024_4938-5257,x_chromosome_mrna_for_ccg1_protein_invin_cell_proliferation
 x16504cds_781-1266:in_reversesequence,_1283-1354,eno3_mrna_for_beta-enolase_(ec_4.2.1.11).

Metagene 258

30 ab000816_783-1357,mrna_for_bmal1d,_partial_cds/gb=ab000816_/ntype=rna
 d17716_1820-2390,mrna_for_n-
 acetylglucosaminyltransferase_v,_complete_cds/gb=d17716_/ntype=rna_
 d25539_3997-4375,mrna_for_kiaa0040_gene,_complete_cds
35 hg742-ht742_at_hg742-ht742_latent_membrane_protein_lmp1
 l07597_2496-3036,ribosomal_protein_s6_kinase(rps6ka2)_mrna,_complete_cds_
 m10014cds#1_1048-1264:in_reversesequence,_9512-9722,fibrinogen_gamma_chain_and_gamma-
 prime_chain_gen
 m28825_1513-2047,thymocyte_antigen_cd1a_mrna,_complete_cds_

u03274_1497-1941,biotinidase_mrna,_complete_cds
u51241cds_717-1029:in_reversesequence,_1257-
1497,eosinophil_eotaxin_receptor_(cmkbr3)_gene,_complete
all_x63755_579-994,mrna_for_high-sulphur_keratin_
5 x80343cds_435-807:in_reversesequence,_1006-
1036,p35_mrna_for_regulatory_subunit_of_cdk5_kinase
all_x83929_2707-3257,mrna_for_typedesmocollin_

Metagene 280

10
u60665_1603-2149,testis_specific_basic_protein_(tsbp),_complete_cds

Metagene 248

15 m16474mrna_1788-2223,fetal_butyrylcholinesterase_mrna,_complete_cds
u25433_2428-
2842:not_in_gb_record,protein_associated_with_tumorigenic_conversion_(catr1.3)_mrna,_com
u59423_1481-1943,smad1_mrna,_complete_cds
x76538_433-931,mpv17_mrna

20
Metagene 416

all_m16404_1576-2153,m2_muscarinic_acetylcholine_receptor_gene_
m73746_2409-2894,lutropin/choriogonadotropin_receptor_(lhgr)_mrna,_complete_cds

25
Metagene 3

j00117mrna_9-428,chorionic_gonadotropin_(hcg)_beta_subunit_mrna,_complete_cds
m12759cds_65-335:in_reversesequence,_1020-1260,ig_j_chain_gene
30 all_m85220_15-
201,heavy_chain_disease_iga_chain_gene,_ch3_region_with_a_369_bp_deletion,_3'_end
s71043mrna_442-
970,_ig_alpha_2=immunoglobulin_a_heavy_chain_allotype{constant_region,_germ_line}_[_hu
u24152_1879-2215,p21-activated_protein_kinase_(pak1)_gene,_complete_cds
35 all_x60992_2450-3021,cd6_mrna_for_t_cell_glycoprotein_cd6

Metagene 472

h46990_40-
 355,_yo16d02.s1cdna_clone_178083_3'_similar_to_gb:j02625_cytochrome_p450_iie1_(human);
 m86873mrna_155-367,type_a_plasminogen_related_gene_
 s42303_3537-4029,_n-cadherin_[human,_umbilical_vein_endothelial_cells,_mrna,_4132_nt]
 5 all_z80776_596-795,h2a/g_gene

Metagene 457

d10202_1209-1557,mrna_for_platelet-activating_factor_receptor,_complete_cds
 10 d13643_3585-4131,mrna_for_kiaa0018_gene,_complete_cds
 d49387_401-917,mrna_for_nadp_dependent_leukotriene_b4_12-
 hydroxydehydrogenase,_partial_cds/gb=d49387
 hg4606-ht5011_at_hg4606-ht5011_centractin_alpha_
 j03890mrna#1_482-1022:not_in_gb_record,_sp-c1_gene_(pulmonary_surfactant_protein_sp-
 15 c)_extracted_fro
 k03195_2303-2813,(hepg2)_glucose_transporter_gene_mrna,_complete_cds_
 113210_1668-2214,mac-2_binding_protein_mrna,_complete_cds
 120348exon_15-219:not_in_gb_record,oncomodulin_gene
 142563mrna_3011-3443,(clone_lsw34)_non-gastric_h,k-atpase_(atp1all1)_gene
 20 m27504_2078-2626,topoisomerase_type_ii_(topo_ii)_mrna,_partial_cds/gb=m27504_/ntype=mrna_
 m28215_130-676,gtp-binding_protein_(rab5)_mrna,_complete_cds
 u20648_316-766,zinc_finger_protein_(znf154)_mrna,_partial_cds
 y00318cds#1_1317-1653:in_reversesequence,_1814-
 1916,mrna_for_complement_control_protein_factor_i
 25 all_z15108_1535-2130,mrna_for_protein_kinase_c_zeta

Metagene 443

ab000468_2302-2860,mrna_for_zinc_finger_protein,_clone_res4-26,_complete_cds_
 30 ab002533_1726-2128,mrna_for_qip1,_complete_cds
 reverse_ac002077_3475-3730,cosmid_clone_luca17_from_3p21.3_
 ad000092cds#2_714-1008:in_fullsequence,_87557-87797,_hypotheticalserine-
 threonine_protein_kinase_r31
 d16480_2089-2641,mrna_for_mitochondrial_enoyl-coa_hydratase/3-hydroxyacyl-
 35 coa_dehydrogenase_alpha-su
 d38552_1532-2012,mrna_for_kiaa0073_gene,_partial_cds_
 d63475_1309-1819,mrna_for_kiaa0109_gene,_complete_cds
 d63477_4745-5243,mrna_for_kiaa0143_gene,_partial_cds_
 d79206exon#5_1513-2053,gene_for_ryudocan_core_protein,_exon1-5,_complete_cds_

d85245_1248-1806,mrna_for_tr3beta,_complete_cds
 all_d87017_16956-
 20256,_c7_segment_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_
 d87116_1514-2048,mrna_for_map_kinase_kinase_3b_,complete_cds_
 5 hg2290-ht2386_at_hg2290-ht2386_calcitonin
 hg2755-ht2862_at_hg2755-ht2862_t-plastin_
 hg2887-ht3031_at_hg2887-ht3031_sry-related_hmg-boxprotein
 hg331-ht331_at_hg331-ht331_tenascin
 hg3897-ht4167_at_hg3897-ht4167_sodium_channel_type_iii_alpha_subunit_brain
 10 hg3925-ht4195_s_at_hg3925-ht4195_surfacant_protein_sp-a2_delta_
 j02906mrna_1254-1782,cytochrome_p450iifl_protein_(cyp2f)_mrna,_complete_cds
 i25444_2124-2694,(tafii70-alpha)_mrna,_complete_cds_
 m22960mrna_1352-1760,protective_protein_mrna,_complete_cds_
 m24439exon_492-912,liver/bone/kidney-type_alkaline_phosphatase_(alpl)_gene_
 15 m60284cds_835-1144:in_reversesequence,_251-479,neurokinin_a_receptor_(nk-2r)_gene_
 m68941mrna_3078-3618,protein-tyrosine_phosphatase_mrna,_complete_cds_
 m91669_4061-4636,bullous_pemphigoid_autoantigen_bp180_gene,_3'_end_
 m92303_3057-3633,voltage-dependent_calcium_channel_beta-1_subunit_mrna,_complete_cds_
 m95623exon#14-15_2-
 20 383:not_in_gb_record,_pbgd_gene_(hydroxymethylbilane_synthase)_extracted_fromhydr
 s38742_1370-1835,_hox11=hox11_homeodomain_{homeobox}_[_human,_mrna,_1988_nt]_
 s65583mrna_588-1068,_sp-10=intra-
 acrosomal_protein_{alternatively_spliced}[_human,_liver,_genomic,_2
 s87759_1823-2321,_protein_phosphatase_2c_alpha[_human,_teratocarcinoma,_mrna,_2346_nt]
 25 u01337exon#16_412-553,ser/thr_protein_kinase_(a-raf-1)_gene,_complete_cds
 u04898_1421-1877,orphan_hormone_nuclear_receptor_roralpha2_mrna,_complete_cds
 u11292_2353-2863,ki_nuclear_autoantigen_mrna,_complete_cds_
 u15655_2102-2576,ets_domain_protein_erf_mrna,_complete_cds_
 u25034_588-1127,neuronatin_beta_mrna,_complete_cds_
 30 u25956mrna_1470-2046,p-selectin_glycoprotein_ligand_(selplg)_gene
 u30894_2068-2626,n-sulphoglucosamine_sulphohydrolase_mrna,_complete_cds
 u32439_1324-1822,regulator_of_g-protein_signaling_similarity_(rgs7)_mrna,_partial_cds
 u32674cds_593-1060:in_reversesequence,_1181-
 1191,orphan_receptor_gpr9_(gpr9)_gene,_partial_cds
 35 u39573_2173-2689,salivary_peroxidase_mrna,_complete_cds
 u40391mrna_464-980,serotonin_n-acetyltransferase_gene,_complete_cds_
 u40434_1561-2071,mesothelin_or_cak1_antigen_precursor_mrna,_complete_cds_
 u42031_1655-2201,54_kda_progestrone_receptor-
 associated_immunophilin_fkbp54_mrna,_partial_cds_

u43374_775-1069,normal_keratinocyte_mrna_
 u45973_1634-2192,phosphatidylinositol_(4,5)bisphosphate_5-
 phosphatase_homolog_mrna,_partial_cds
 u46751_1562-
5 2012,phosphotyrosine_independent_ligand_p62_for_the_lck_sh2_domain_mrna,_complete_cds
 u49857_314-749,transcriptional_activator_mrna,_complete_cds
 u50330_3071-3515,procollagen_c-proteinase_(pcp-2)_mrna,_complete_cds_
 u68111mrna_858-1374,protein_phosphatase_inhibitor(ppp1r2)_gene
 u70671_695-1115,ataxin-2_related_protein_mrna,_partial_cds_
10 u72206_3122-3590,guanine_nucleotide_regulatory_factor_(lfp40)_mrna,_complete_cds_
 u92457_2832-3375,metabotropic glutamate_receptormrna,_complete_cds
 x05855cds_12-65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
 all_x07290_1212-1723,hf.12_gene_mrna_
 all_x07767_1948-2516,mrna_for_camp-
15 dependent_protein_kinase_catalytic_subunit_type_alpha_(ec_2.7.1.3
 all_x07948_3-428,mrna_for_transition_protein(tp1)
 x59932mrna_1557-2063,mrna_for_c-src-kinase_
 all_x66945_3582-3931,n-sam_mrna_for_fibroblast_growth_factor_receptor
 x78687exon#6_172-670,g9_gene_encoding_sialidase
20 x79865cds_267-411:in_reversesequence,_922,mrp17_mrna
 x81372cds_701-791:in_reversesequence,_1027-1195,mrna_for_biphenyl_hydrolase-related_protein
 all_x89066_3817-4019,mrna_for_trpc1_protein
 all_x91504_970-1523,mrna_for_arp1_protein
 all_x94232_2035-2528,mrna_for_novel_t-cell_activation_protein
25 all_x98482_45-
 72,tnnt2_gene_exon/gb=x98482_/ntype=dna_annot=mrna,tnnt2_gene_exon/gb=x98482_/ntype=d
 all_z12962_31-398,mrna_for_homologue_to_yeast_ribosomal_protein_141
 z22548cds_310-547:in_reversesequence,_684-894,thiol-specific_antioxidant_protein_mrna_
 z73497cds_28-
30 229,dna_sequence_from_cosmid_u240c2,_between_markers_dxs366_and_dxs87_on_chromosome_x
 co

Metagene 430

35 d87458_3244-3784,mrna_for_kiaa0282_gene,_partial_cds_
 m99564_2505-2991,(clone_dn10mel)_p_protein_mrna,_complete_cds_

Metagene 426

d30037_609-1179,mrna_for_phosphatidylinositol_transfer_protein_(pi-tpbeta),_complete_cds_
 all_j03027_3437-3996,mhc_i_hla-6.09_gene,_complete_cds_
 all_m14306_171-361,beta-a3/a1-crystallin_gene_(hu-beta-a3/a1)
 all_m30703_55-142:not_in_gb_record,amphiregulin_(ar)_gene_
5 u14407_601-1147,interleukin(il15)_mrna,_complete_cds_
 u33054_1584-2010,g_protein-
 coupled_receptor_kinase_grk4_mrna,_alpha_splice_variant,_complete_cds_
 x94629_618-1128,mrna_for_metaphase_chromosomal_protein
 y10518mrna_138-648,mrna_for_cd202_protein/gb=y10518_ntype=rna_
10 z83804_29-261,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc7).

Metagene 406

15 u06454_1832-2288,amp-activated_protein_kinase_(hampk)_mrna,_complete_cds_
 all_y00705_5-356,ptsi_mrna_for_pancreatic_secretory_inhibitor_(expressed_in_neoplastic_tissue)

Metagene 393

j03474cds_3-255,serum_amyloid_a_gene,_complete_cds_
20 all_m63262_161-540:in_m63262cds_231-340,5-lipoxygenase_activating_protein_(flap)_gene_
 all_x51441_55-90,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clone_pas3-
 alpha,mrna_for_serum_amy
 x75042cds_1607-1817:in_reversesequence,_2024-2252,rel_proto-oncogene_mrna_

25 Metagene 381

af005361_1159-1663,importin_alpha_mrna,_complete_cds/gb=af005361_ntype=rna_
 hg3731-ht4001_r_at_hg3731-ht4001_immunoglobulin_heavy_chain,_vdjrc_regions_
 l38616mrna_1184-1634,brain_and_reproductive_organ-
30 expressed_protein_(bre)_gene,_complete_cds
 u46746_1183-1708,dystrobrevin-epsilon_mrna,_complete_cds_
 all_u61500_6060-6577,gt334_protein_(gt334)_gene_mrna,_complete_cds_

Metagene 361

35
 m16364_749-1311,creatine_kinase-b_mrna,_complete_cds_
 m64554mrna_1602-
 1962_f13a1_gene_(coagulation_factor_xiib)_extracted_fromfactor_xiii_b_subunit_gene
 u07794_cds2_at_u07794_u07794,not_in_gb_record,tyrosine_kinase_(tkk)_gene

Metagene 357

hg3432_ht3620_s_at_hg3432_ht3620_fibroblast_growth_factor_receptor_k-sam,_altslice_3,_k-
 5 sam_iii_
 s79048_61-421,_lprp=phl_e1f1_[human,_lacrimal_gland,_mrna_partial,_507_nt]
 u39657_2341-2863,map_kinase_kinase(mkk6)_mrna,_complete_cds_
 u97188_3602-4010,putative_rna_binding_protein_koc_(koc)_mrna,_complete_cds
 x66417cds_230-524:in_reversesequence,_658-766,cask_mrna_for_kappa-casein

10

Metagene 354

aj000480cds_116-650,mrna_for_c8fw_phosphoprotein/gb=aj000480_/ntype=rna_
 d21241exon#2_2-72,_ovary- and prostate-specific_exonfromcytochrome_p-
 15 450_aromatase_gene,_multiple_ex
 d30742_1211-1697,mrna_for_calmodulin-dependent_protein_kinase_iv,_complete_cds_
 d80011_4259-4793,mrna_for_kiaa0189_gene,_complete_cds
 hg1980-ht2023_at_hg1980-ht2023_tubulin,_beta_2_
 hg2264-ht2360_at_hg2264-ht2360_atpase,_ca2+_transporting,_plasma_membrane_1,_altslice_6_
 20 hg273-ht273_at_hg273-ht273_lymphocyte_antigen_hla-g3_
 hg3517-ht3711_at_hg3517-ht3711_alpha-1-antitrypsin,_5'_end_
 hg620-ht620_at_hg620-ht620_tyrosine_phosphatase,_epsilon_
 l05424_cds2_at_l05424_105424,not_in_gb_record,_cd44_gene_(cell_surface_glycoprotein_cd44)_ex-
 tracted_
 25 110844_1646-2213,cellular_growth-regulating_protein_mrna,_complete_cds_
 114848_802-1181,mhc_i-related_protein_mrna,_complete_cds_
 l28957_685-1231,ctp:phosphocholine_cytidyltransferase_mrna,_complete_cds
 all_m23178_2889-3818,homologue-
 1_of_gene_encoding_alpha_subunit_of_murine_cytokine_(mip1/sci),_compl
 30 m27436mrna_1638-
 1979,tissue_factor_gene,_complete_cds,_with_a_alu_repetitive_sequence_in_the_3'_untr
 m27819_3060-3426,anion_exchange_protein(ae1,_band_3)_mrna,_complete_cds_
 m33318mrna_1538-1583,cytochrome_p450iiia3_(cyp2a3)_mrna,_complete_cds_
 m62324_1584-2052,modulator_recognition_factor_i_(mrf-1)_mrna,_3'_end_
 35 u30888_1892-2420,trna-guanine_transglycosylase_mrna,_complete_cds
 u40571_1695-2073,alpha1-syntrophin_(snt_a1)_mrna,_complete_cds_
 u82310_19-229,unknown_protein_mrna,_partial_cds/gb=u82310_/ntype=rna_
 u82818_1005-1058,ucp3s_mrna,_complete_cds/gb=u82818_/ntype=rna
 u84551_cds2_at_u84551_u84551,not_in_gb_record,dystrobrevin_(dtn)_gene_-

x03934cds_255-423:in_reversesequence,_3890-4112,t-cell_antigen_receptor_gene_t3-delta_
 all_x07619_658-1162,mrna_for_cytochrome_p450_db1_variant_b_
 x12458mrna_1566-2046,_p3_protein_(aa_1-1382)_gene_extracted_fromp3_gene_
 all_x13967_3247-3806,mrna_for_leukaemia_inhibitory_factor_(lif/hilda)

5 x16901cds_411-711:in_reversesequence,_866-
 1094,mrna_for_rap30_subunit_of_transcription_initiation_fa
 x52599cds_295-649,mrna_for_beta_nerve_growth_factor
 x94563mrna#1_109-
 123,_exon_1b; used_only_in_type transcripts_fromdbi/acbp_gene_exon&/gb=x94563_/ntype

10 y10506mrna_251-593,mrna_for_cd110_protein/gb=y10506_/ntype=rna_
 y10615cds_115-535,cyrn2_gene/gb=y10615_/ntype=dna_/annot=cds_
 all_z46632_2953-3206,hspde4c1_gene_for_3',5'-
 cyclic_amp_phosphodiesterase,hspde4c1_gene_for_3',5'

15 Metagene 346

u45974_1007-1517,phosphatidylinositol_(4,5)_bisphosphate_5-
 phosphatase_homolog_mrna,_partial_cds_
 u79304_1102-1630,clone_23909_mrna,_partial_cds.

20 x05839mrna_2298-
 2467,_transforming_growth_factor_beta precursor_gene_extracted_fromtransforming_growt

Metagene 340

25 l34838_40-586,early_placenta_insulin-like_peptide_epil_(insl4)_mrna,_complete_cds_
 all_u05255_159-188,glycophorin_hep2_mrna,_partial_cds,glycophorin_hep2_mrna,_partial_cds
 u31501_2359-
 2773,fragile_x_mental_retardation_syndrome_related_protein_(fxr2)_mrna,_complete_cds_
 u37689_344-752,rna_polymerase_ii_subunit_(hsrbp8)_mrna,_complete_cds_
 30 x15943mrna_884-1220:in_reversesequence,_7046-7076,_huamn_calcitonin/alpha-cgrp_gene

Metagene 336

35 u08021_447-909,nicotinamide_n-methyltransferase_(nnmt)_mrna,_complete_cds
 all_x83107_1867-2348,bmx_mrna_for_cytoplasmic_tyrosine_kinase

Metagene 333

u96191_19-439,trophoblast_hypoxia-regulated_factor-5_(hrf-
 5)_mrna,_3'_end/gb=u96191_/ntype=rna_
 all_x13955_675-827,mrna_for_myosin_alkali_light_chain
 x64877cds_417-762:in_reversesequence,_889-
5 894,mrna_for_serum_protein,mrna_for_serum_protein

Metagene 322

hg2229-ht2306_at_hg2229-ht2306_paired_box_hup1_
10 m54914exon_1099-1666,follicle-stimulating_hormone_beta-subunit_gene

Metagene 267

hg544-ht544_at_hg544-ht544_endothelial_cell_growth_factor_
15 105072exon#10_375-907,interferon_regulatory_factorgene,_complete_cds_
 107261mrna_283-
 505,alpha_adducin_mrna,_partial_cds_including_alternate_exons_a_and_b_(trimmed_to_889
 137360_146-698,(clone_hehk1-l)_ehk1_receptor_tyrosine_kinase_ligand_(efl-
 2)_mrna,_complete_cds
20 177567mrna_947-1231,mitochondrial_citrate_transport_protein_(ctp)_mrna,_3'_end
 m25667_1086-1200,neuronal_growth_protein_43_(gap-43)_mrna,_complete_cds
 m32886_351-843,sorcincp-22_mrna,_complete_cds
 u07151_395-869,gtp_binding_protein_(arl3)_mrna,_complete_cds
 u29175_5199-5223,transcriptional_activator_(brg1)_mrna,_complete_cds.
25 u30827_1253-1817,splicing_factor_srp40-3_(srp40)_mrna,_complete_cds
 u30999_25-379,(memc)_mrna,_3'_utr/gb=u30999_/ntype=rna_
 u51432_1557-2079,nuclear_protein_skip_mrna,_complete_cds.
 u53830_1469-1835,interferon_regulatory_factor_7a_mrna,_complete_cds_
 u60873_115-439,clone_137308_mrna,_partial_cds
30 u79261_883-1422,clone_23959_mrna,_partial_cds
 all_x14813_1077-1618,liver_mrna_for_3-oxoacyl-coa_thiolase_
 x64177cds_8-147:in_reversesequence,_2-277,mrna_for_metallothionein
 x94333_1617-2157,mrna_for_tgn46_protein
 x97074cds_182-398:in_reversesequence,_704-782,mrnas_for_clathrin-associated_protein
35 z46376mrna_4703-5249,hk2_mrna_for_hexokinase_ii_

Metagene 264

d21239_3475-3997,mrna_for_c3g_protein,_complete_cds

d49958_1830-2346,fetus_brain_mrna_for_membrane_glycoprotein_m6,_complete_cds_
d88613_1068-1518,mrna_for_hgcma,_complete_cds
d88667_1298-1652,mrna_for_cerebroside_sulfotransferase,_complete_cds_
hg1098-ht1098_at_hg1098-ht1098_cystatin_d

5 hg2161-ht2231_at_hg2161-ht2231_translocation-associated_notch_(drosophila)_homolog
hg2191-ht2261_at_hg2191-ht2261_crystallin,_beta_b3_
hg3477-ht3670_at_hg3477-ht3670_cd4_antigen_
hg3928-ht4198_at_hg3928-ht4198_surfacant_protein_sp-a1_delta_
hg4336-ht4606_at_hg4336-ht4606_bactericidal_bpi'gene_

10 hg4535-ht4940_s_at_hg4535-ht4940_dematin_
j02888_453-915,quinone_oxidoreductase_(nqo2)_mrna,_complete_cds
k03008cds_90-118:not_in_gb_record,_gamma-g2-psi_gene_extracted_fromgamma-c-
crystallin_(gamma-3)_gene
111372_497-893,protocadherin_43_mrna,_3'_end_of_cds_for_alternative_splicing_pc43-12_

15 117327_16-196,pre-t/nk_cell_associated_protein_(3b3)_mrna,_3'_end
140904mrna_1228-
1656,_hsapiens_peroxisome_proliferator_activated_receptor_gamma,_complete_cds_
m12625mrna_893-1259:in_reversesequence,_1599-1683,lecithin-
cholesterol_acyltransferase_mrna,_complet

20 m14123cds#1_263-665,_pol_fromendogenous_retrovirus_herv-
k10/gb=m14123_/ntype=dna/_annot=cds,_pol_fro
all_m16707_590-
631,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_clone_f
m21302_402-514,small_proline_rich_protein_(sprii)_mrna,_clone_174n_

25 m21904cds_1189-1549:in_reversesequence,_372-
378,4f2_glycosylated_heavy_chain_(4f2hc)_antigen_gene_
m61733_2454-2934,erythroid_membrane_protein_4.1_mrna,_complete_cds
m90366_1683-2175,zona_pellucida_glycoprotein(zp2)_mrna,_complete_cds
m91585_3719-4175,br140_mrna,_complete_cds

30 s80267_1304-1872,_p72syk_{g_insertion_nucleotide_92}_[human,_jurkat_e6-
1_j.cam1_cells,_mrna_partial_
u01120_2484-2982,glucose-6-phosphatase_mrna,_complete_cds
u04270_3505-3973,putative_potassium_channel_subunit_(h-erg)_mrna,_complete_cds_
u07856cds#5_1300-1846,endogenous_retrovirus_in_complement_c4a_gene,_a3_allele,_herv-

35 k(c4)_(_gag),(_po
u11090_733-1243,hydroxyindole-o-methyltransferase_promoter_a-
derived_(hiomt)_mrna,_complete_cds
u13666cds_671-989:in_reversesequence,_1329-1413,g_protein-
coupled_receptor_(gpr1)_gene,_complete_cds

u18244_1166-1640,excitatory_amino_acid_transportermrna,_complete_cds
 u18543_1853-2339,zinc-finger_protein_mrna,_complete_cds
 all_u19107_3423-3658,znf127_(znf127)_gene,_complete_cds_
 u19977_735-1227,preprocarboxypeptidase_a2_(procpa2)_mrna,_complete_cds_
5 u20582_1180-1690,actin-like_peptide_mrna,_partial_cds
 u20657_2439-2890:not_in_gb_record,ubiquitin_protease_(unph)_proto-
 oncogene_mrna,_complete_cds_
 u31342mrna_1173-1629,nucleobindin_gene_
 u33317mrna_25-421,defensin(hd-6)_gene,_complete_cds
10 u33761_1017-1557,cyclin_a/cdk2-associated_p45_(skp2)_mrna,_complete_cds
 u36501_1704-2148,sp100-b_(sp100-b)_mrna,_complete_cds
 u43148_6015-6483,patched_homolog_(ptc)_mrna,_complete_cds
 u48263_627-1173,pre-pro-orphanin_fq_(ofq)_mrna,_complete_cds_
 u49973cds#1_764-
15 1340,_orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtrigger1_transpos
 u59878_469-895,low-mr_gtp-binding_protein_(rab32)_mrna,_partial_cds
 u76010_1520-1964,putative_zinc_transporter_znt-3_(znt-3)_mrna,_complete_cds
 u77845_1515-1905,htrip_(htrip)_mrna,_complete_cds
 u78793_6-29,folate_receptor_alpha_(hfr)_mrna,_partial_cds/gb=u78793/_ntype=rna_
20 u86759_1374-1856,netrin-2_like_protein_(ntn2l)_mrna,_complete_cds
 all_u90543_2501-
 2545,butyrophilin_(btfl)_mrna,_complete_cds,butyrophilin_(btfl)_mrna,_complete_cds
 u95019_2358-2862,voltage-dependent_calcium_channel_beta-2c_subunit_mrna,_complete_cds
 all_x04297_3519-4090,mrna_for_na,k-atpase_alpha-subunit
25 all_x05246_1045-1556,testis-specific_pgk-2_gene_for_phosphoglycerate_kinase_(atp:3-phospho-d-
 glycera
 all_x53800_377-961,mrna_for_macrophage_inflammatory_protein-2beta_(mip2beta)_
 x76942cds_24-420:in_reversesequence,_487-527,mrna_for_72.1_protein
 x92518mrna_4077-4127,mrna_for_hmgi-c_protein_
30 x96783mrna_1442-2015,syt_v_gene_(genomic_and_cdna_sequence)_
 ,all_x97058_1042-1565,mrna_for_p2y6_receptor
 y08200_1496-2006,mrna_for_rab_geranylgeranyl_transferase,_alpha-subunit
 all_z71460_2546-3033,mrna_for_vacuolar-type_h(+)atpase_115_kda_subunit

35 Metagene 255

 d10922_1288-1808,mrna_for_fmlp-related_receptor_(hm63)_
 m11567mrna_188-620,angiogenin_gene,_complete_cds,_and_three_alu_repetitive_sequences

Metagene 253

ab002356_5330-5807,mrna_for_kiaa0358_gene,_complete_cds/gb=ab002356/_ntype=rna_111701_2320-2609,phospholipase_d_mrna,_complete_cds

5 142374mrna_1836-2389,pp2a_b56-beta_mrna,_complete_cds_m19508exon#1_2-98,_mpo_frommyeloperoxidase_gene,_exons_1-4/gb=m19508/_ntype=dna/_annot=exon_all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-hydroxylase_(cyp11b1)

10 m81182_2831-3314,peroxisomal_70_kd_membrane_protein_mrna,_complete_cds_u25975_1675-1795,serine_kinase_(hpak65)_mrna,_partial_cds_u47686_2174-2747,signal_transducer_and_activator_of_transcription_stat5b_mrna,_complete_cds_all_u67092_1093-1868:not_in_gb_record,ataxia-telangiectasia_locus_protein_(atm)_gene,_exons_1a,_1b,

15 all_x16609_6641-7241,mrna_for_ankyrin_(variant_2.1)_x51953exon#1-2_37-64:not_in_gb_record,ucp_gene_for_uncoupling_protein_exonsand/gb=x51953/_ntype=dna_all_x52228_1631-2103,mrna_for_secreted_epithelial_tumour_mucin_antigen_x58528mrna_2689-3193,pmp70_mrna_for_a_peroxisomal_membrane_protein

20 x95808mrna_5503-6037,mrna_for_protein_encoded_by_a_candidate_gene,_dxs6673e,_for_mental_retardation_z11899cds_446-706:in_reversesequence,_989-1074,otf3_mrna_encoding_octamer_binding_protein_3b_z22951mrna_717-1231,of_p65_gene_encoding_p65_subunit_of_transcription_factor_nf-kappab_

25 reverse_z68280_34936-35175,dna_sequence_from_cosmid_125a3,_huntington's_disease_region,_chromosome_4

Metagene 172

30 m22430_300-732,rasf-a_pla2_mrna,_complete_cds_u80669_863-1403,androgen_regulated_homeobox_protein_(nkx3.1)_mrna,_complete_cds_z70222cds_3-213:in_reversesequence,_25-37,mrna_for_orf_(clone_icrfp507g2490)

Metagene 123

35 d90064_1806-2184,cgm6_mrna_for_cd66b_(nca-95) m87507_751-1177:in_reversesequence,_1012-1130,_homo_sapien_interleukin-1_beta_convertase_(il1bce)_mr m91556_4785-5343,voltage-gated_sodium_channel_mrna,_complete_cds.

u82275_1335-1647,immunoglobulin-like_transcriptmrna,_complete_cds_x15675mrna_1522-1840,ptr7_mrna_for_repetitive_sequence/gb=x15675_/ntype=rna

Metagene 119

5

d00003_1681-1981,liver_cytochrome_p-450_mrna,_complete_cds,liver_cytochrome_p-450_mrna,_complete_cds

m74047_1878-2316,steroid_5-alpha-reductase(srd5a2)_mrna,_complete_cds_s53911_2110-

10 2584,_cd34=glycoprotein_expressed_in_lymphohematopoietic_progenitor_cells_{alternatively u42360mrna_867-1346,n33_gene x54867mrna_783-1293,mrna_for_nkg2-a_gene_ x65663cds_83-137,sox-6_mrna/gb=x65663_/ntype=rna_ y11174cds_48-516:in_reversesequence,_600,mrna_for_rp3_gene/gb=y11174_/ntype=rna_

15

Metagene 118

d12620_1535-1965,mrna_for_cytochrome_p-450ltbv_

d38522_3436-3958,mrna_for_kiaa0080_gene,_partial_cds_

20 d63861exon#10_90-656,dna_for_cyclophilin_40,_complete_cds

hg831-ht831_at_hg831-ht831_potassium_channel_

j02883mrna_55-493,colipase_mrna,_complete_cds

140393mrna_1754-2222,(clone_s171)_mrna,_complete_cds

m94172_6837-7328,n-type_calcium_channel_alpha-1_subunit_mrna,_complete_cds_

25 u05589_877-1453,ribosomal_protein_s1_homolog_mrna,_partial_cds_

u08854_1612-2040,udp glucuronosyltransferase_precursor_(ugt2b15)_mrna,_complete_cds

u16954_1099-1579,(aflq)_mrna,_complete_cds_

u17327_6523-7081,neuronal_nitric_oxide_synthase_(nos1)_mrna,_complete_cds

u35637_8831-9367,nebulin_mrna,_partial_cds/gb=u35637_/ntype=rna

30 u47926_1546-1996,unknown_protein_b_mrna,_complete_cds

u90546_1301-

1344,butyrophilin_(btf4)_mrna,_complete_cds,butyrophilin_(btf4)_mrna,_complete_cds

x02158mrna_949-1219,gene_for_erythropoietin_

all_x06562_3951-4396,mrna_for_growth_hormone_receptor

35 x14474cds_669-710,mrna_for_microtubule-associated_tau_protein

all_x86400_560-1155,mrna_for_gamma_subunit_of_sodium_potassium_atpase

all_x98176_772-1022,mrna_for_mach-beta-1_protein/gb=x98176_/ntype=rna

z69030cds_838-1186,mrna_for_gammaisoform_of_61kda_regulatory_subunit_of_pp2a

Metagene 112

j04621mrna_2879-3347,heparan_sulfate_proteoglycan_(hspg)_core_protein,_3'_end
 all_m27749_245-348,immunoglobulin-related_14.1_protein_mrna,_complete_cds,immunoglobulin-
5 related_14.
 all_x51730_4462-5003,mrna_and_promoter_dna_for_progesterone_receptor_

Metagene 89

10 hg2139-ht2208_f_at_hg2139-ht2208_beta-1-glycoprotein_1,_pregnancy-specific_-
 m22403exon#2_1749-2224,blood_platelet_membrane_glycoprotein_ib-
 alpha_(gpib)_gene,_complete_cds,_clon
 u31201_cds1_at_u31201_u31201,not_in_gb_record,laminin_gamma2_chain_gene_(lамc2),laminin_-
 gamma2_chain
15 u73167cds#4_1050-1254:in_reversesequence,_13521-
 13767:not_in_gb_record,_h_luca14.2a_gene_extracted_f
 x58288mrna_4517-4955,hr-ptpu_gene_for_protein_tyrosine_phosphatase_-
 all_x66276_3221-3734,mrna_for_skeletal_muscle_c-protein

20 Metagene 78

af005887_1969-
 2413,atf_family_member_atf6_(atf6)_mrna,_complete_cds/gb=af005887_/ntype=rna
 d00860_1546-2020,mrna_for_phosphoribosyl_pyrophosphate_synthetase_(ec_2.7.6.1)_subunit_i_-
25 d13370exon#5_193-637,apx_gene_encoding_apex_nuclease,_complete_cds_-
 d50550_3217-3475,llgl_mrna,_complete_cds_-
 d85131_1126-1679,mrna_for_myc-associated_zinc-finger_protein_ofislet,_complete_cds_-
 d87989_597-1095,mrna_for_udp-galactose_transporter_related_isozyme_1,_complete_cds_-
 hg982-ht982_s_at_hg982-ht982_pre-t/nk-cell-associated_protein_1f6
30 j03263_667-1218,lysosome-associated_membrane_glycoprotein_(lamp_a)_mrna,_complete_cds_-
 l04282_1873-2329,caccc_box-binding_protein_mrna,_complete_cds_-
 l15189_1520-2081,mitochondrial_hsp75_mrna,_complete_cds_-
 l25876_359-785,protein_tyrosine_phosphatase_(cip2)mrna,_complete_cds_-
 l43579_6-
35 403,(clone_110298)_mrna/gb=l43579_/ntype=rna,(clone_110298)_mrna/gb=l43579_/ntype=rna
 m24766_1513-2055,(clone_phai2-12)_alpha-2_collagen_type_iv_(col4a2)_mrna,_3'_end
 m31169cds_2-71,propionyl-coa_carboxylase_beta-subunit_(beta-
 pcc)_gene,_partial_cds_(mutant_delta-atc)
 m34423_1856-2312,beta-galactosidase_(glb1)_mrna,_complete_cds_-

m36429_827-1412,transducin_beta-2_subunit_mrna,_complete_cds_
m60891mrna_6-411,uroporphyrinogen_decarboxylase_(uro-
d)_gene,_partial_cds/gb=m60891/_ntype=dna/_anno
m94250exon#4-5_43-301:not_in_gb_record,retinoic_acid_inducible_factor_(mk)_gene_exons_1-
5 _complete_
u10323_963-1467,nuclear_factor_nf45_mrna,_complete_cds_
u14417_567-1017,ral_guanine_nucleotide_dissociation_stimulator_mrna,_partial_cds_
u28963_567-1143,gps2_(gps2)_mrna,_complete_cds_
u29171_1340-1742,casein_kinase_i_delta_mrna,_complete_cds

10 u35835_2404-2859,dna-pk_mrna,_partial_cds
u47105_616-1174,h105e3_mrna,_complete_cds
u50553_2647-3079,helicase_like_proteinmrna,_complete_cds
u61734cds_461-628:in_reversesequence,_710-
767,protein_trafficking_protein_(s31iii125)_mrna,_complete

15 u72935mrna#1_7752-
7898,_atrx_gene_(putative_dna_dependent_atpase_and_helicase)_extracted_fromputativ
u73477_440-885,acidic_nuclear_phosphoprotein_pp32_mrna,_complete_cds_
u78722_1523-1965,zinc_finger_protein_165_(zpf165)_mrna,_complete_cds
u81802_2557-3043,ptdins_4-kinase_(pi4kb)_mrna,_complete_cds

20 x54199mrna_2616-3006:in_reversesequence,_3118,mrna_for_gars-airs-gart_
x55448exon#13_150-670,_g6pd_gene_(glucose-6-
phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
x55544cds_350-626:in_reversesequence,_984-1110,cdna_for_treb_protein
x55885mrna_587-1049,mrna_for_a_presumptive_kdel_receptor_
25 x58521cds_1250-1544:in_reversesequence,_1701-1785,mrna_for_p62_nucleoporin
x66397cds_6605-6977:in_reversesequence,_7352-7442,tpr_mrna
all_x66503_1125-1690,adenylosuccinate_synthetase_mrna
all_x78925_1966-2447,hzf2_mrna_for_zinc_finger_protein_
x90872cds_288-600:in_reversesequence,_799,mrna_for_gp2512_protein_
30 z49107cds_619-947:in_reversesequence,_1046-1259,mrna_for_galectin_
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z97054cds#2_428-
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35 Metagene 58
x02544cds_256-544:in_reversesequence,_688-772,mrna_for_alpha1-
acid_glycoprotein_(orosomucoid)_
all_x78932_421-976,hzf9_mrna_for_zinc_finger_protein_

CLAIMS

What is claimed is:

1. A classification tree model incorporating Bayesian analysis for the statistical prediction of binary outcomes.
- 5 2. The tree model of claim 1, wherein the prediction of a binary outcome is dependent on the interaction of data comprising at least two predictor variables.
3. The tree model of claim 2, wherein the data arises by case control design such that the number of 0/1 values in the response data is fixed by design.
- 10 4. The tree model of claim 3, such that the case control design assesses association between predictors and binary outcome with nodes of a tree.
5. The tree model of claim 4, such that the Bayesian analysis comprises using sequences of Bayes factor based tests of association to rank and select predictors that define a node split.
- 15 6. The tree model of claim 5, further comprising the forward generation of at least one class of trees with high marginal likelihood, wherein the prediction of said class of trees is conducted using principles of model averaging.
7. The tree model of claim 6, wherein the principle of model averaging comprises the steps of:
 - 20 weighted prediction of a tree by determining its implied posterior probability by a score;
 - evaluation of the score to exclude unlikely trees;
 - evaluation of the posterior and predictive distribution at each node and leaf of a tree; and
- 25 application of said posterior and predictive distribution to the evaluation o of each tree and the averaging of predictions across trees for future predictive cases.
8. The tree model of claim 1 or 2, wherein the binary outcome is a clinical state.
9. The tree model of claim 1 or 2, wherein the binary outcome is a physiological state.
- 30 10. The tree model of claim 1 or 2, wherein the binary outcome is a physical state.
11. The tree model of claim 1 or 2, wherein the binary outcome is a disease state.

12. The tree model of claim 1 or 2, wherein the binary outcome is a risk group.
13. The tree model of claim 1 or 2, wherein the data is biological data.
14. The tree model of claim 1 or 2, wherein the data is statistical data.

Figure 1

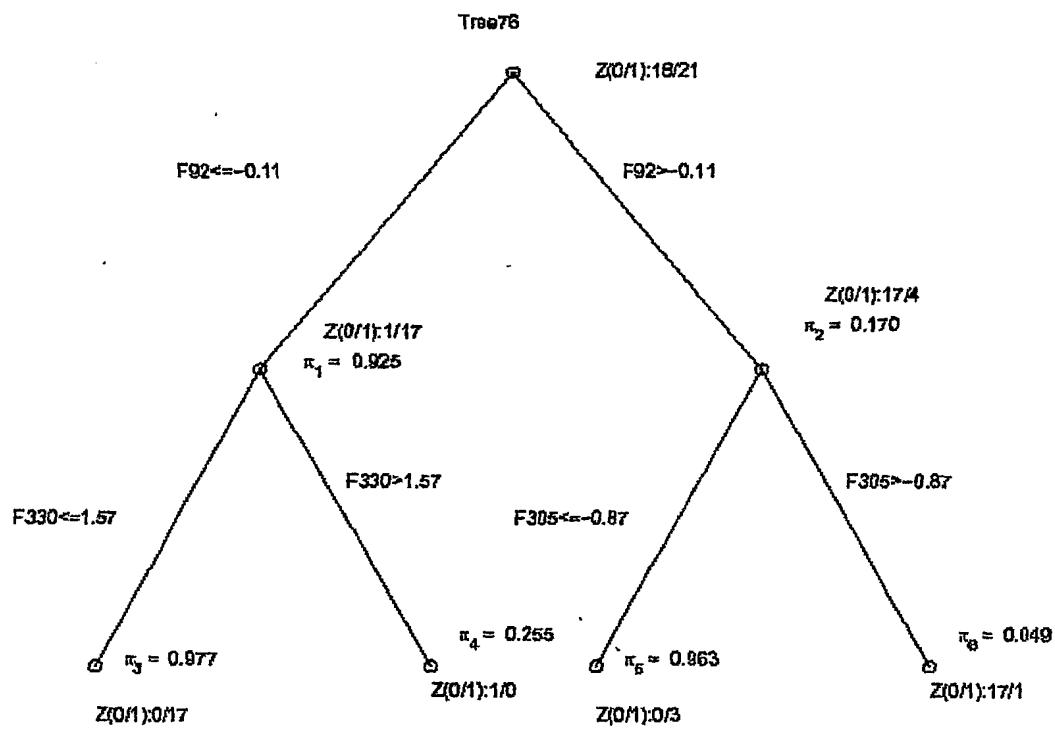


Figure 2

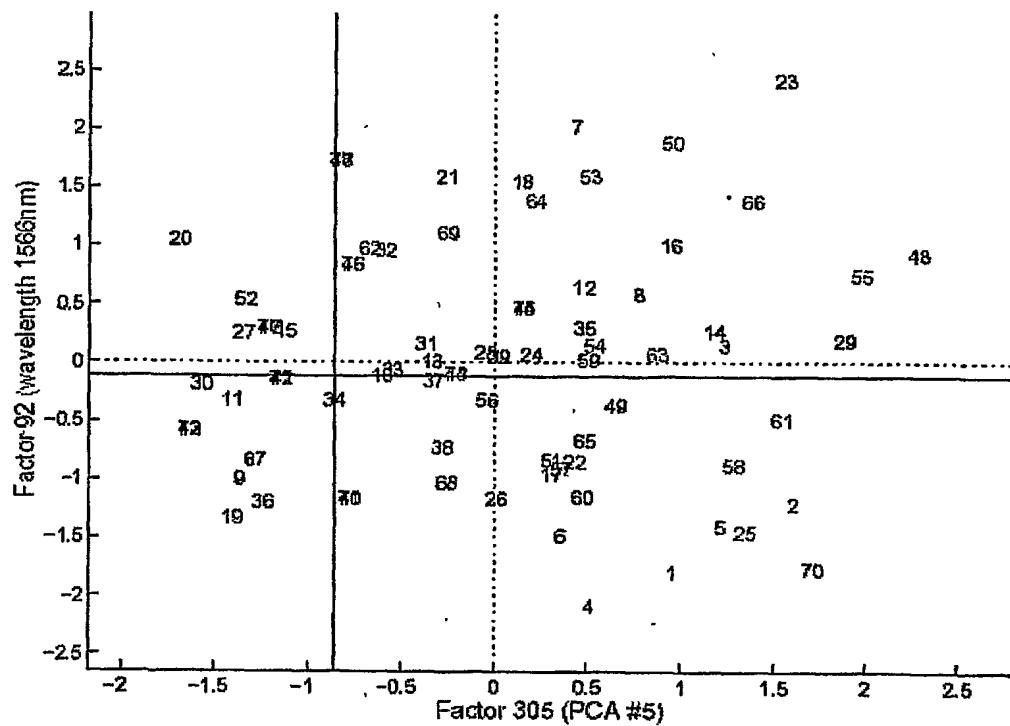


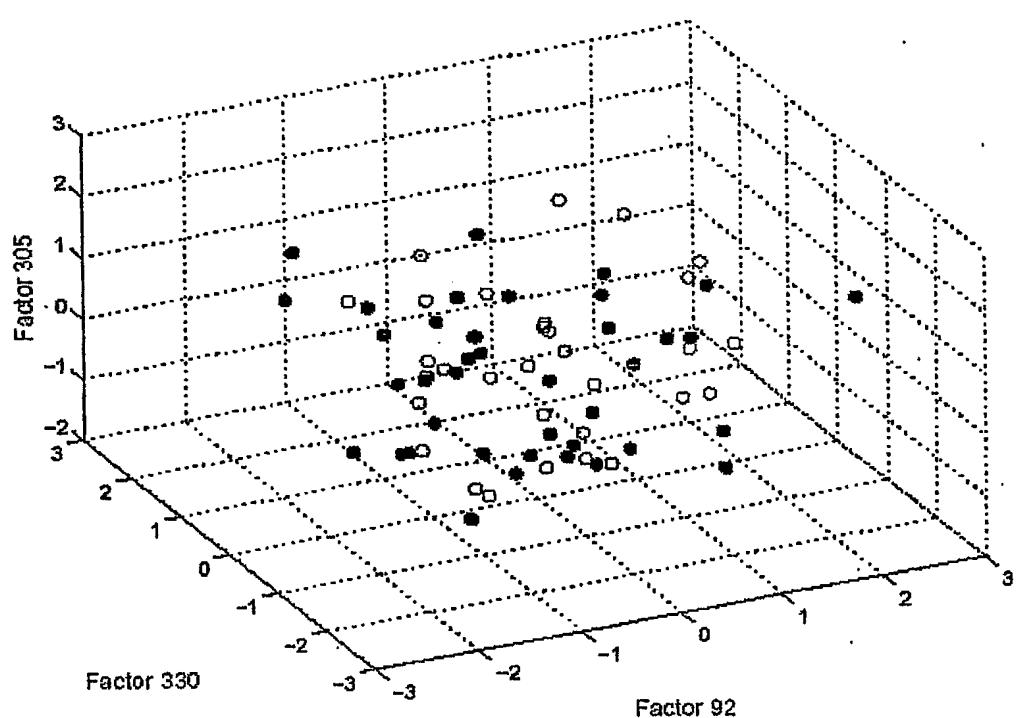
Figure 3

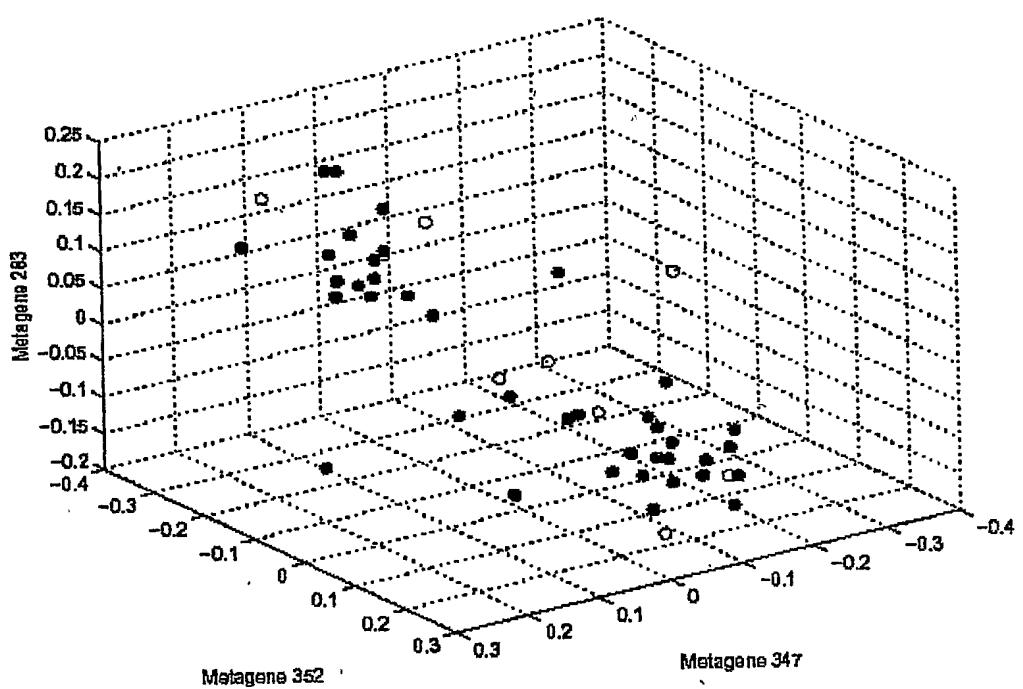
Figure 4

Figure 5

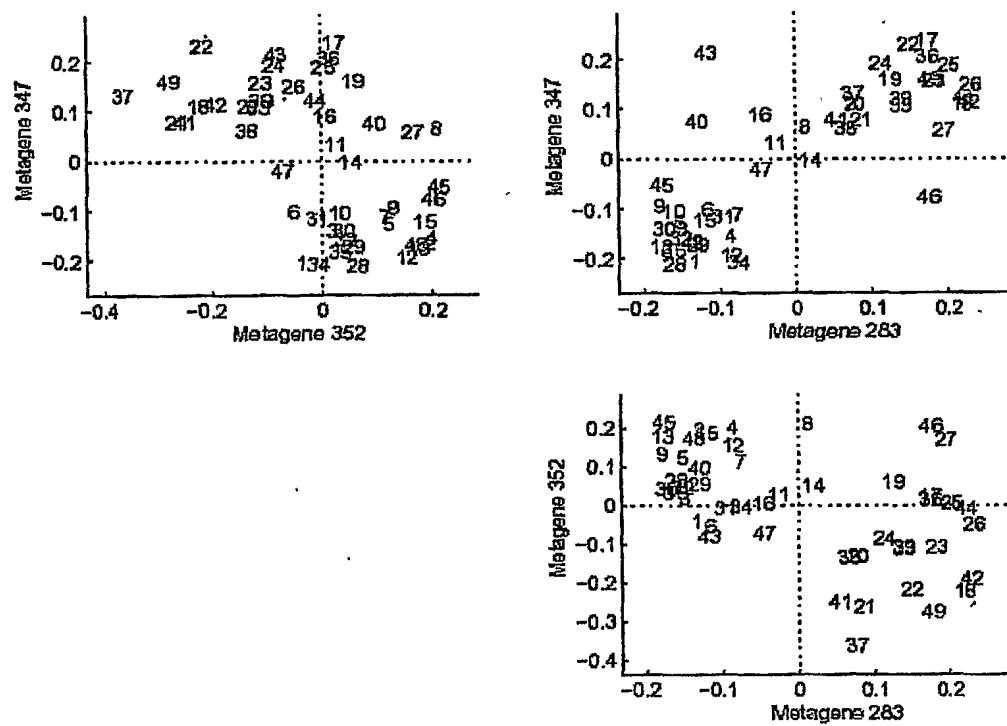


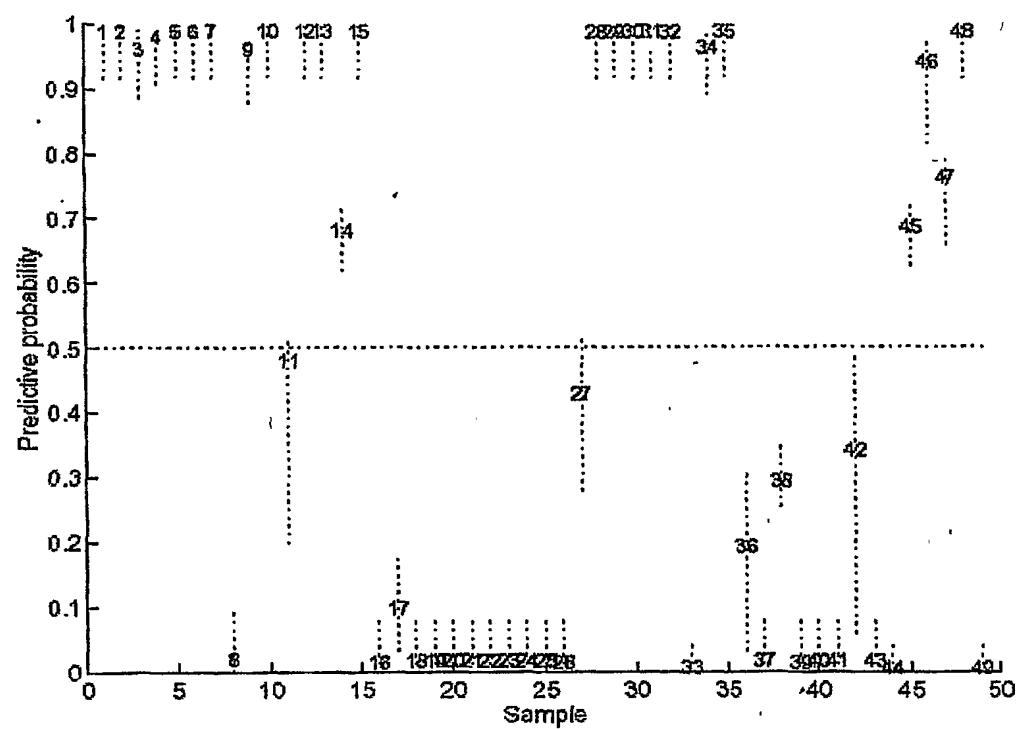
Figure 6

Figure 7

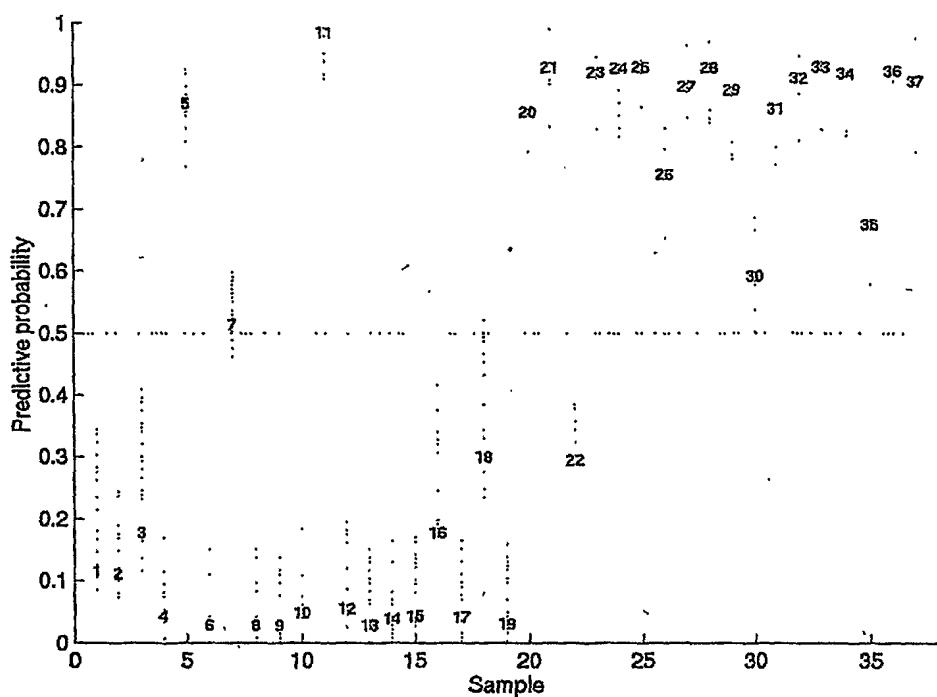


Figure 8

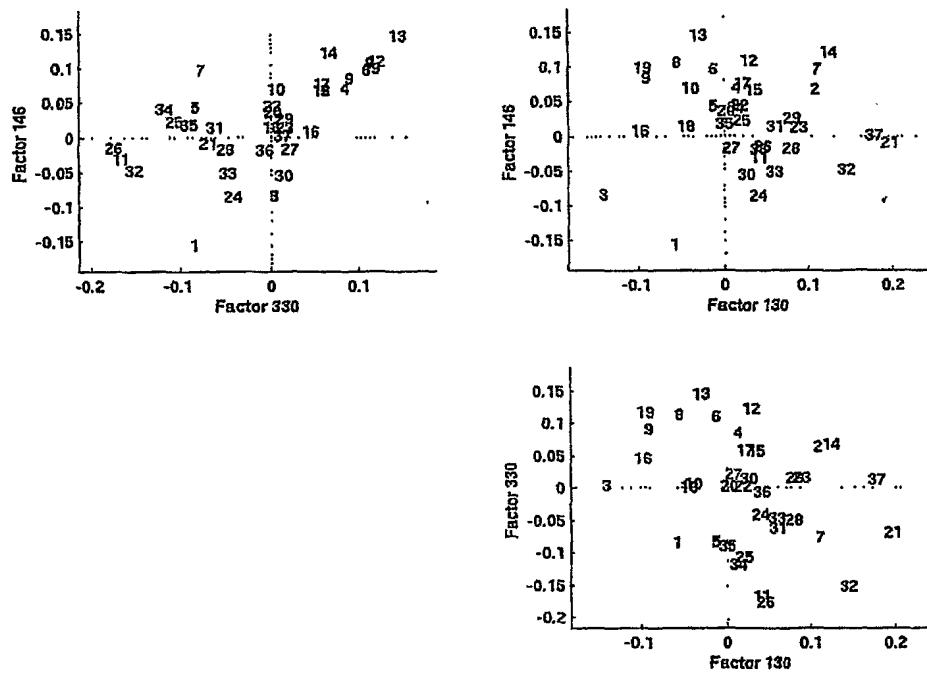


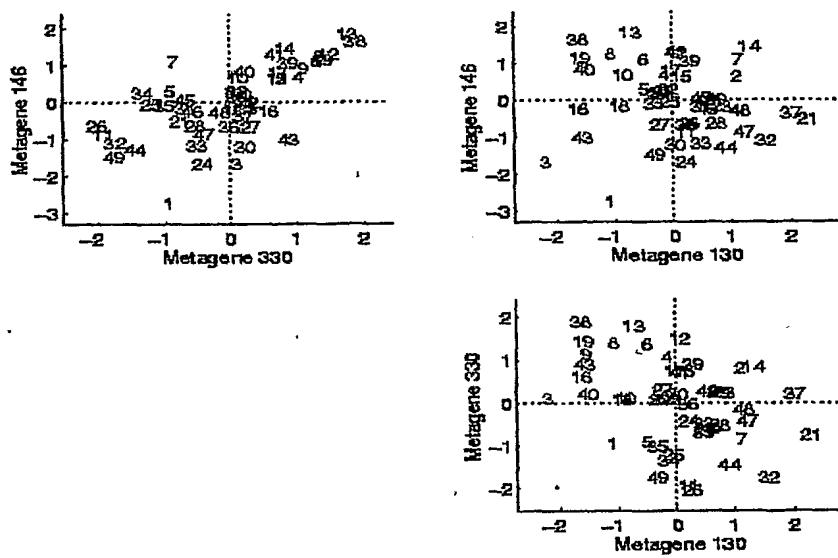
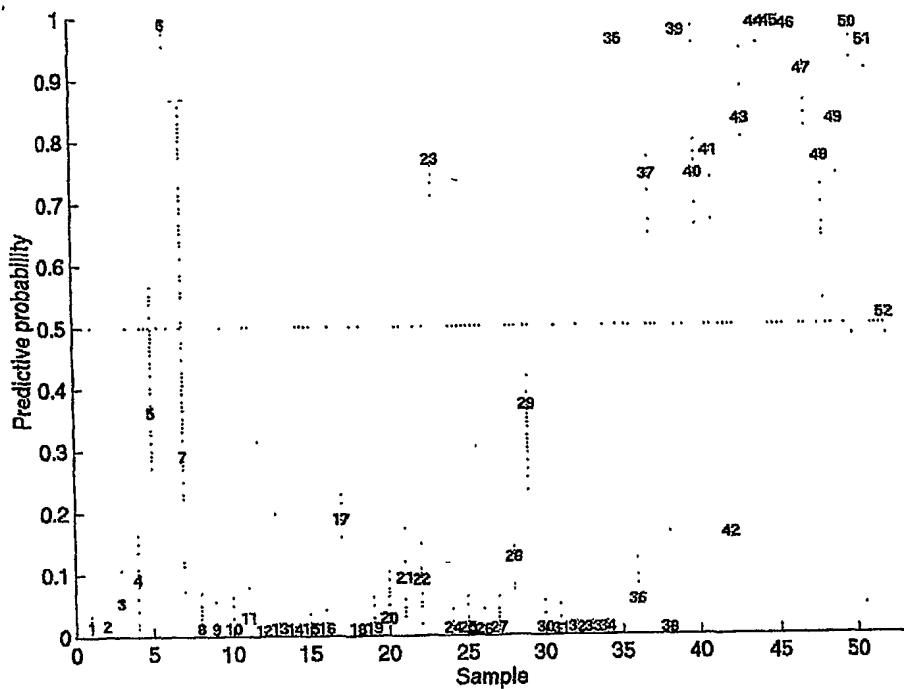
Figure 9

FIG. 10



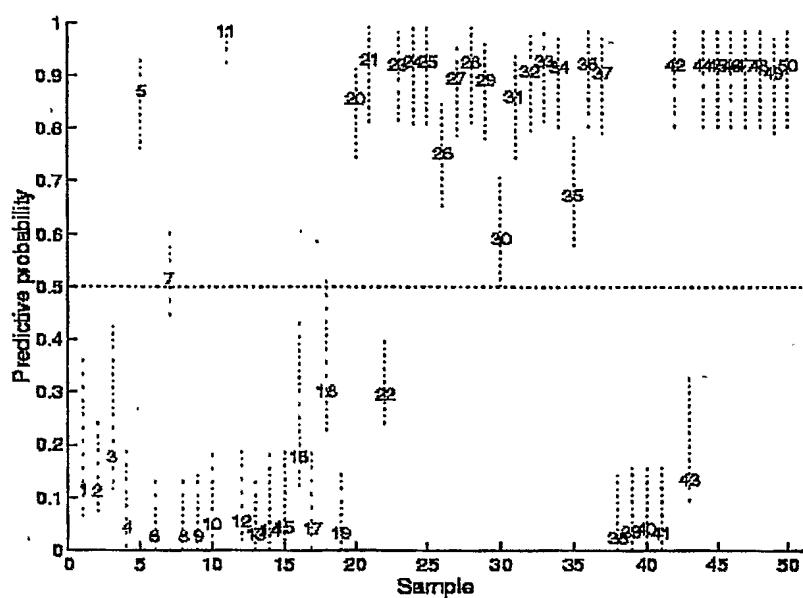


Figure 11

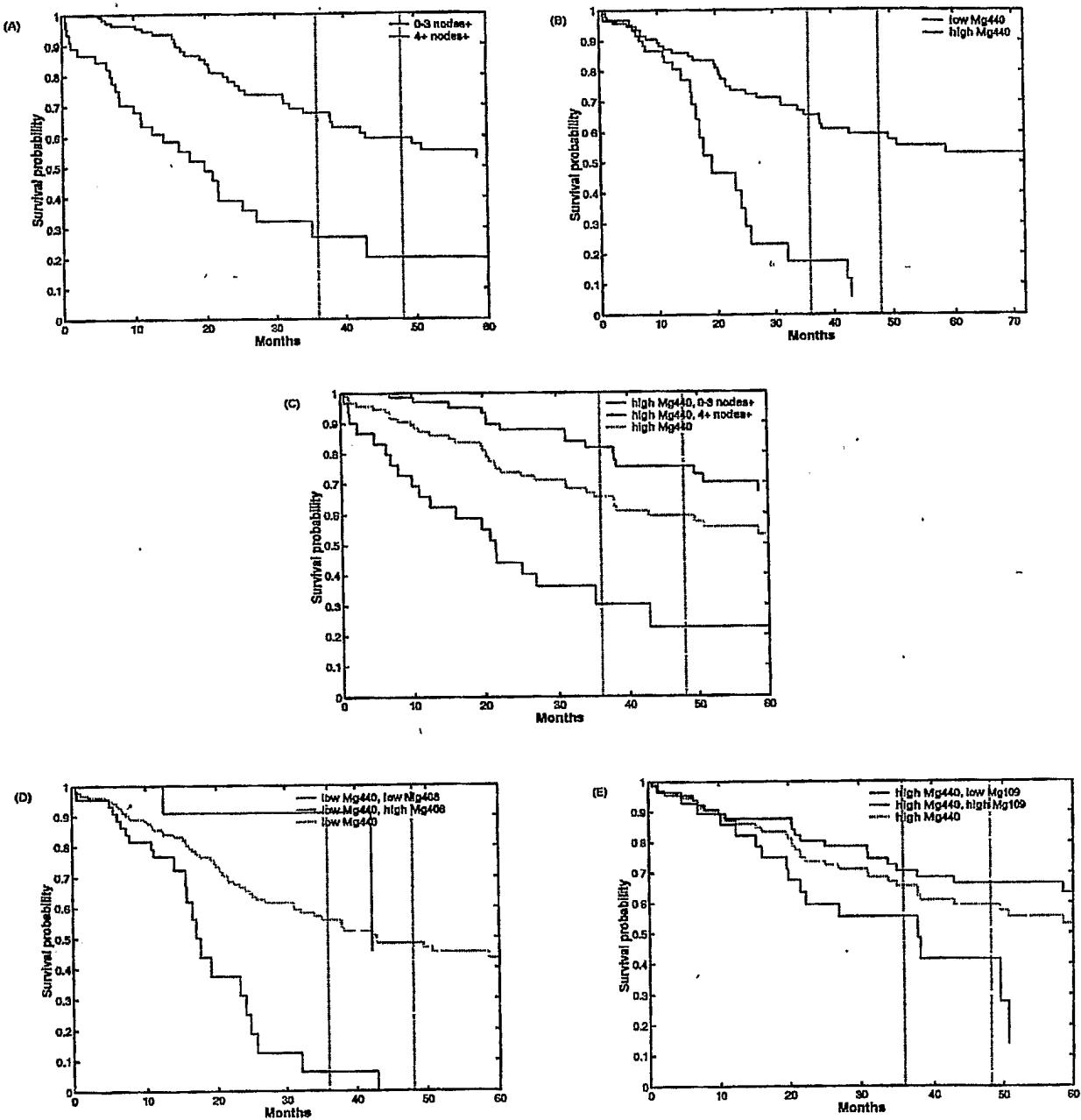
FIGURE 12.

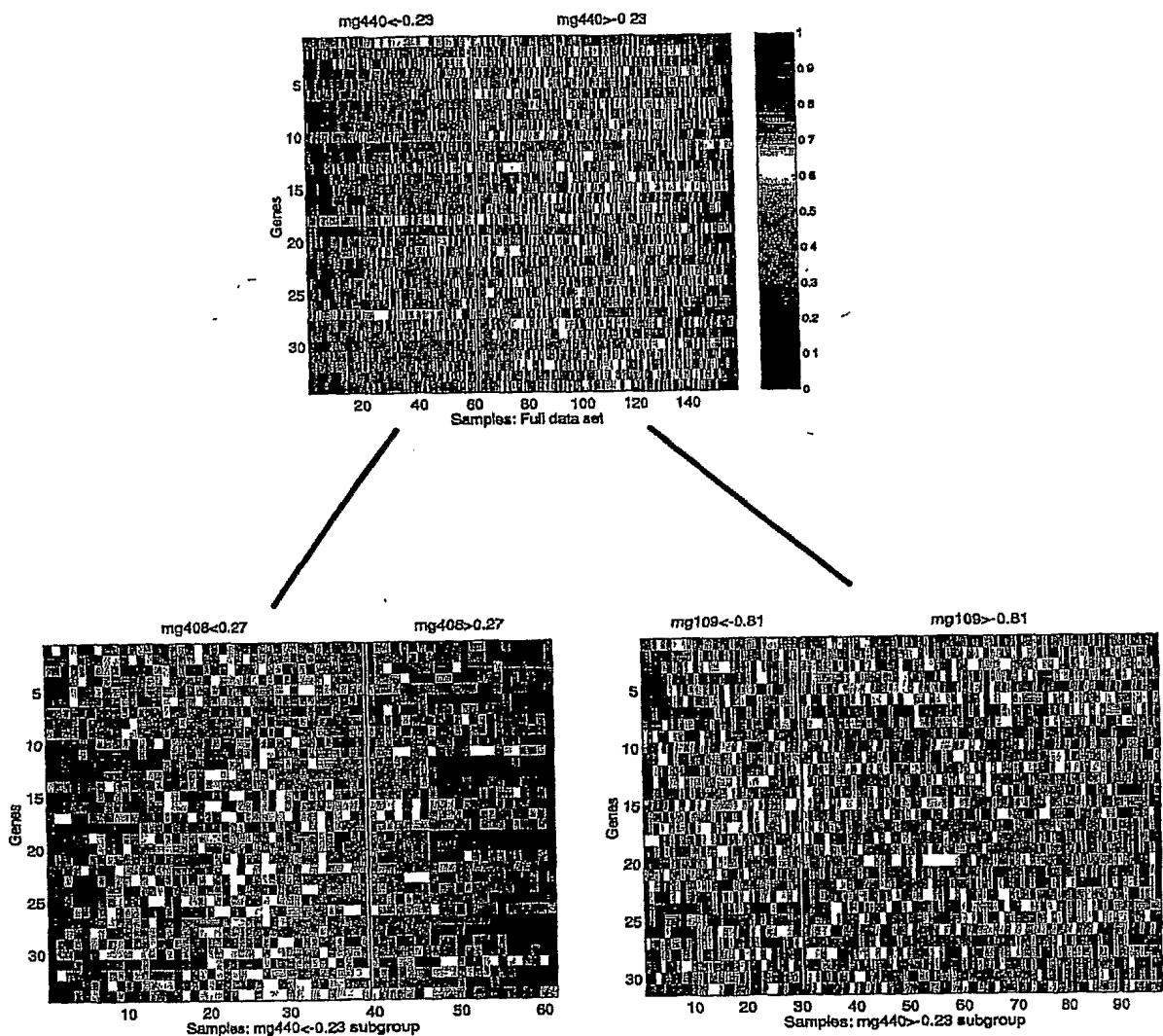
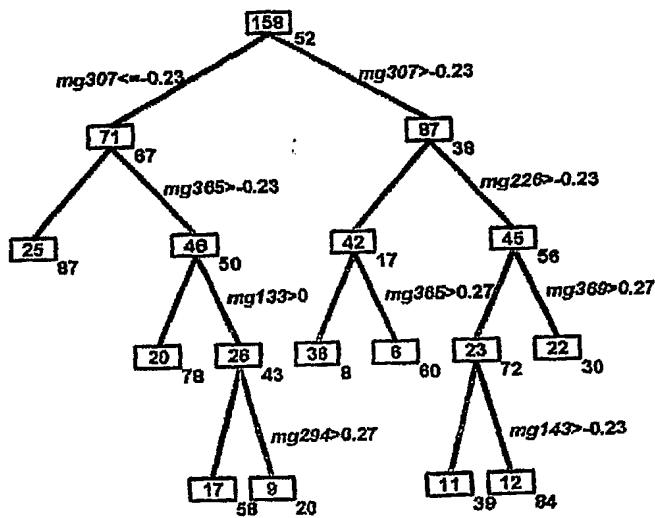
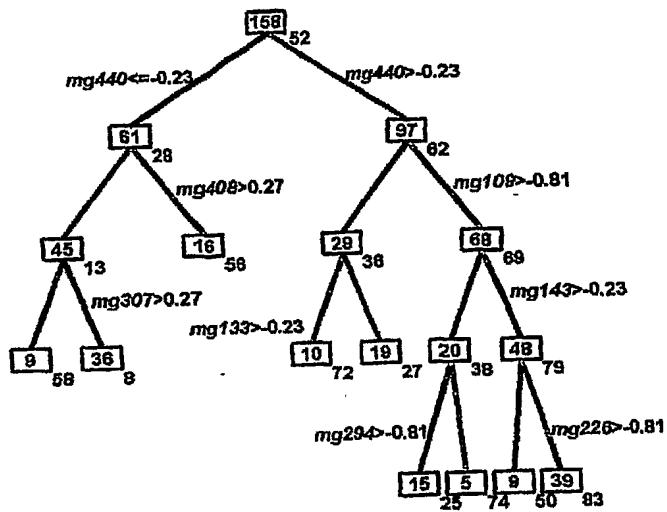
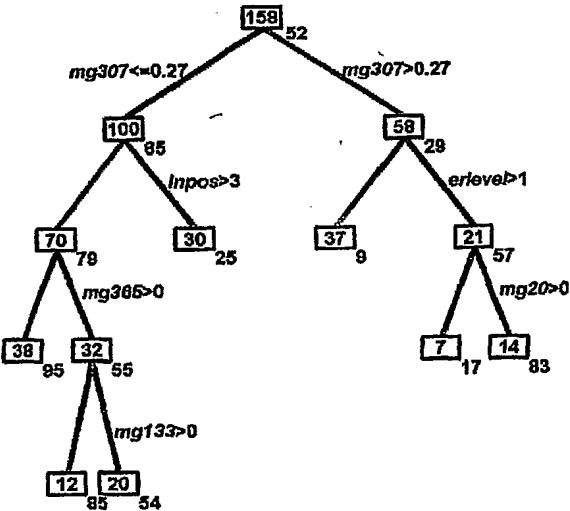
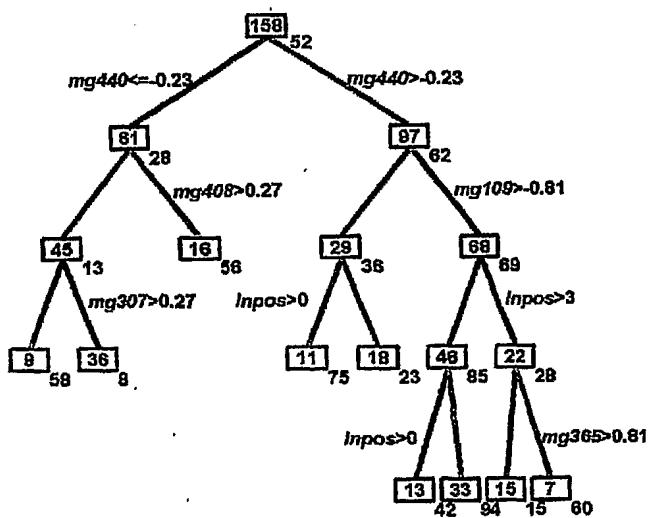
FIGURE 13

FIGURE 8(A)



14
FIGURE 6(B)



15
FIGURE 4(A)

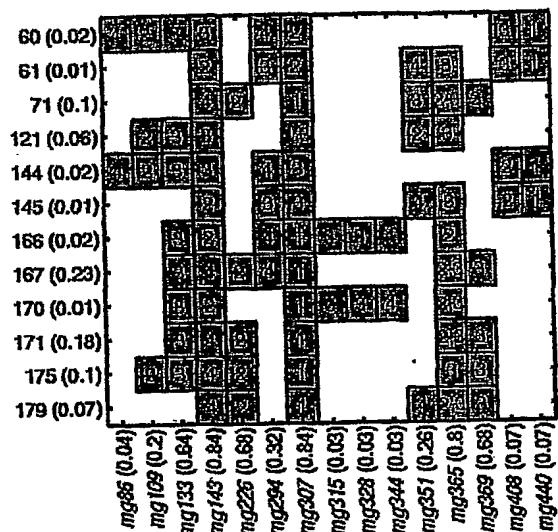


FIGURE 4(B)

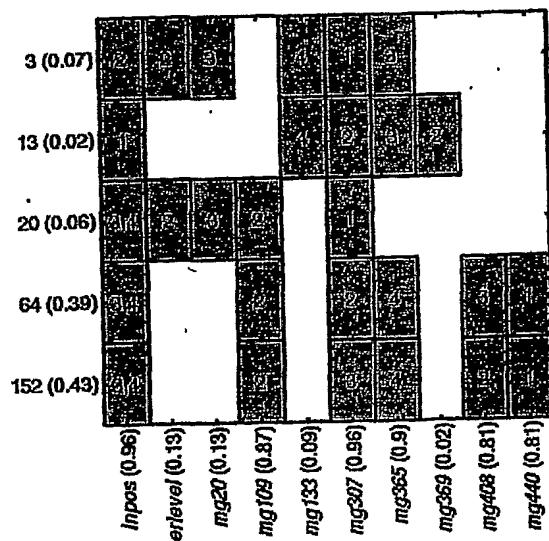


FIGURE 16(A)

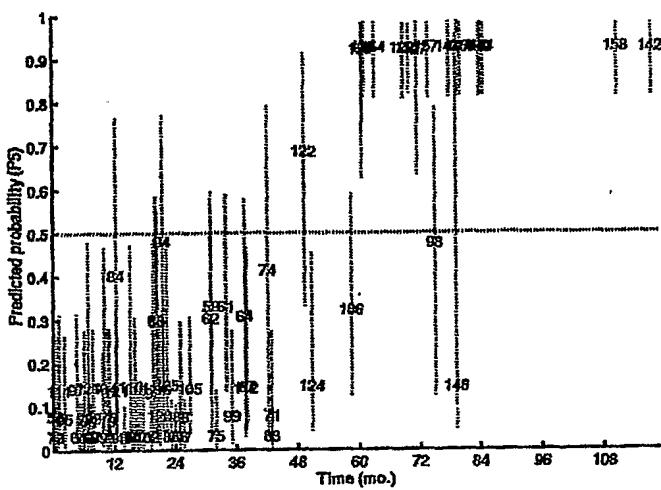
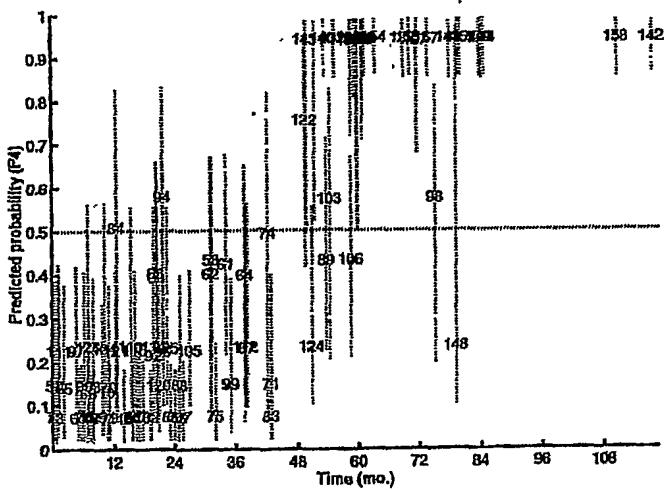


FIGURE 5(B)



17
FIGURE •

